GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 18, 2003, 04:12:19 ; Search time 44.4279 Seconds
(without alignments)
5391.080 Million cell updates/sec

Title: US-09-026-459A-37
Perfect score: 4017
Sequence: 1 MSRLLKKYDVLFALFSKLER.....TRMQKQKMNDSMDTSNKEEK 781

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4017	100.0	2994	1	US-08-204-329-2	Sequence 2, Appli
2	4017	100.0	2994	2	US-08-482-627-4	Sequence 4, Appli
3	4017	100.0	2994	3	US-08-801-092-3	Sequence 3, Appli
4	4017	100.0	2994	4	US-09-315-113-3	Sequence 3, Appli
5	4017	100.0	2995	2	US-08-959-638-7	Sequence 7, Appli
6	4017	100.0	3232	1	US-08-038-760-1	Sequence 1, Appli
c 7	4017	100.0	3232	1	US-08-038-760-2	Sequence 2, Appli
8	4017	100.0	3232	2	US-08-470-091-1	Sequence 1, Appli
c 9	4017	100.0	3232	2	US-08-470-091-2	Sequence 2, Appli
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11	4007	99.8	2995	4	US-08-328-673A-7	Sequence 7, Appli
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13	763	19.0	2808	2	US-08-152-721B-1	Sequence 1, Appli
14	729.5	18.2	4853	1	US-08-832-883-1	Sequence 1, Appli
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16	727.5	18.1	3249	1	US-08-106-493A-1	Sequence 1, Appli
17	727.5	18.1	3249	1	US-08-429-264-1	Sequence 1, Appli
18	516.5	12.9	3747	4	US-09-213-293D-2	Sequence 2, Appli
19	144	3.6	6773	4	US-09-166-350-27	Sequence 27, Appl
20	143.5	3.6	3763	1	US-07-792-865D-1	Sequence 1, Appli
21	143	3.6	3593	4	US-09-404-627-3	Sequence 3, Appli
22	143	3.6	4205	4	US-09-404-627-1	Sequence 1, Appli
23	140	3.5	8789	1	US-08-328-254-5	Sequence 5, Appli
24	138	3.4	3883	1	US-08-468-036-33	Sequence 33, Appl
25	138	3.4	3883	2	US-08-376-843-33	Sequence 33, Appl
26	138	3.4	3884	4	US-09-541-782-3	Sequence 3, Appli
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28	138	3.4	4868	1	US-08-139-937-12	Sequence 12, Appl
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32	131	3.3	2415	4	US-09-134-001C-2381	Sequence 2381, Ap
33	130	3.2	5893	1	US-08-592-126-54	Sequence 54, Appl
34	130	3.2	5893	2	US-08-687-080-44	Sequence 44, Appl
35	127.5	3.2	5181	1	US-08-257-073-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
; GENERAL INFORMATION:
; APPLICANT: SHEPARD, H. M.
; APPLICANT: WEN, SHU F.
; TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI-P110RB
; TITLE OF INVENTION: MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,329
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05866
; FILING DATE: 14-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RENEE A. FITTS
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 16930-000400US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422

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;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2

Alignment Scores:
Pred. No.:              0              Length:          2994
Score:                  4017.00        Matches:         781
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     1              Gaps:            0

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Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
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Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
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Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
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Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
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Qy     681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
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       741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
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Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
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Qy     781 Lys 781
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Db    2920 AAA 2922
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RESULT 2
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
       ZIP:  92122
     COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4

Alignment Scores:
Pred. No.:                0              Length:          2994
Score:                    4017.00        Matches:         781
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       2              Gaps:            0

US-09-026-459A-37 (1-781) x US-08-482-627-4 (1-2994)

Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
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Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419
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Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

     521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
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Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    781 Lys 781
          |||
Db   2920 AAA 2922

RESULT 3
US-08-801-092-3
; Sequence 3, Application US/08801092
; Patent No. 6074850
;  GENERAL INFORMATION:
;    APPLICANT:  Antelman, Douglas
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wils, Kenneth N.
;    TITLE OF INVENTION:  Tissue Specific Expression of
;    TITLE OF INVENTION:  Retinoblastoma Protein
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,092
;      FILING DATE:  14-FEB-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/751,517
;      FILING DATE:  15-NOV-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  016930-001020
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  703-576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-801-092-3

Alignment Scores:
Pred. No.:                0              Length:          2994
Score:                    4017.00        Matches:         781
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       3              Gaps:            0

US-09-026-459A-37 (1-781) x US-08-801-092-3 (1-2994)

Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
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Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
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Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
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Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
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Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
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Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy     341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy     361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy     381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy     401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy     421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy     441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy     461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy     481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy     501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy     521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy     541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy     561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy     581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559
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Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy     681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy     701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy     721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy     741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy     781 Lys 781
           |||
Db    2920 AAA 2922
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```
RESULT 4
US-09-315-113-3
; Sequence 3, Application US/09315113
; Patent No. 6379927
;   GENERAL INFORMATION:
;        APPLICANT: Antelman, Douglas
;                   Gregory, Richard J.
;                   Wils, Kenneth N.
;        TITLE OF INVENTION: Tissue Specific Expression of
;                            Retinoblastoma Protein
;        NUMBER OF SEQUENCES: 46
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/315,113
;             FILING DATE: 19-May-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/801,092
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fitts, Renee A.
;             REGISTRATION NUMBER: 35,136
;             REFERENCE/DOCKET NUMBER: 016930-001020
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-576-0200
;             TELEFAX: 703-576-0300
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2994 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
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;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-315-113-3

Alignment Scores:
Pred. No.:                0              Length:          2994
Score:                    4017.00        Matches:         781
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       4              Gaps:            0

US-09-026-459A-37 (1-781) x US-09-315-113-3 (1-2994)

Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479
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Qy     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy     341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy     361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy     381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

      401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy     421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy     441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy     461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy     481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy     501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy     521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy     541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy     561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy     581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy     681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy     701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy     721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy     741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy     781 Lys 781
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Db    2920 AAA 2922
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RESULT 5
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
; GENERAL INFORMATION:
; APPLICANT: Gregory, Richard J.
; APPLICANT: Wills, Ken N.
; APPLICANT: Maneval, Daniel C.
; TITLE OF INVENTION: Recombinant Adenoviral Vector and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,638
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,673
; FILING DATE: 25-OCT-1994
; APPLICATION NUMBER: US 08/233,777
; FILING DATE: 19-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/142,669
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CJ 1192
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2995 base pairs
; TYPE: nucleic acid

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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7

Alignment Scores:
Pred. No.:                0              Length:          2995
Score:                    4017.00        Matches:         781
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       2              Gaps:            0

US-09-026-459A-37 (1-781) x US-08-959-638-7 (1-2995)

Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy     341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy     361 SerGlyThrAspLeuSerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy     381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy     401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy     421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy     441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy     461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy     481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy     501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy     521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy     541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy     561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy     581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy     681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy     701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy     721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy     741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy     781 Lys 781
          |||
Db    2920 AAA 2922

RESULT 6
US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA

;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1

Alignment Scores:
Pred. No.:                0              Length:         3232
Score:                    4017.00        Matches:        781
Percent Similarity:       100.00%        Conservative:   0
Best Local Similarity:    100.00%        Mismatches:     0
Query Match:              100.00%        Indels:         0
DB:                       1              Gaps:           0

US-09-026-459A-37 (1-781) x US-08-038-760-1 (1-3232)

Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 183

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 243

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 303

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 363

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 423

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     424 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 483

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     484 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 543

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     544 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 603

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     604 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 663

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     664 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 723

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     724 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 783

Qy     221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     784 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 843

Qy     241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     844 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 903

Qy     261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     904 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 963

Qy     281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    964 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1023

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1083

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1143

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1203

Qy    361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1263

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1323

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1383

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1443

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1444 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1503

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1504 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1563

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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Db   1564 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1623

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1624 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1683

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
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      1684 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1743

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1744 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1803

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1804 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1863

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
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Db   1864 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1923

Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1924 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1983

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1984 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2043

Qy    641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2044 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2103

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2163

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2164 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2223

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2224 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2283

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2284 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2343

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2344 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2403

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2404 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2463

Qy    781 Lys 781
          |||
Db   2464 AAA 2466
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RESULT 7
US-08-038-760-2/c
; Sequence 2, Application US/08038760
; Patent No. 5496731
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,760
; FILING DATE: 19930325
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7409-025-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3232 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA
US-08-038-760-2

Alignment Scores:

Pred. No.:	0	Length:	3232
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-026-459A-37 (1-781) x US-08-038-760-2 (1-3232)

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Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
Db    3113 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 3054

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
Db    3053 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 2994

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
Db    2993 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 2934

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
Db    2933 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 2874

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
Db    2873 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 2814

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
Db    2813 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 2754

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
Db    2753 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 2694

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
Db    2693 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 2634

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
Db    2633 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 2574

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db    2573 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 2514

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
Db    2513 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 2454

Qy     221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
Db    2453 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 2394

Qy     241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
Db    2393 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 2334

Qy     261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
Db    2333 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 2274

Qy     281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
Db    2273 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 2214

Qy     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
Db    2213 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 2154

Qy     321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
Db    2153 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 2094

Qy     341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
Db    2093 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 2034

Qy     361 SerGlyThrAspLeuSerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
Db    2033 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1974

Qy     381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
Db    1973 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1914

Qy     401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
Db    1913 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1854

Qy     421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
Db    1853 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1794

Qy     441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
Db    1793 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1734

Qy     461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
Db    1733 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1674

Qy     481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db    1673 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1614

Qy     501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
Db    1613 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1554

Qy     521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
Db    1553 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1494

Qy     541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
Db    1493 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1434

Qy     561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
Db    1433 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1374

Qy     581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
Db    1373 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1314

Qy     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
Db    1313 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1254

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
Db    1253 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1194

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
Db    1193 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1134

Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
Db    1133 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 1074
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Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 1014

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 954

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 894

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
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Db    893 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 834

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 774

          781 Lys 781
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Db    773 AAA 771
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RESULT 8
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1
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Alignment Scores:
Pred. No.:                0              Length:          3232
Score:                    4017.00        Matches:         781
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       2              Gaps:            0

US-09-026-459A-37 (1-781) x US-08-470-091-1 (1-3232)

Qy      1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 183

Qy     21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 243

Qy     41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 303

Qy     61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 363

Qy     81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 423

Qy    101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 483

Qy    121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 543

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 603

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
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Db    604 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 663

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
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Db    664 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 723

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 783

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 843

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 903

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 963

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1023

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1024 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1083

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1143

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1203

Qy    361 SerGlyThrAspLeuSerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1263

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1323

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1324 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1383

      421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1443

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1444 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1503

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1504 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1563

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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Db   1564 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1623

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1624 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1683

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
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Db   1684 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1743

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
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Db   1744 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1803

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
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Db   1804 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1863

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
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Db   1864 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1923

Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
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Db   1924 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1983

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
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Db   1984 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2043

Qy    641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2044 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2103

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2163

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
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Db   2164 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2223

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
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Db   2224 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2283

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2284 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2343

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2344 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2403

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
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Db   2404 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2463

Qy    781 Lys 781
          |||
Db   2464 AAA 2466

RESULT 9
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2

Alignment Scores:
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Pred. No.:	0	Length:	3232
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-026-459A-37 (1-781) x US-08-470-091-2 (1-3232)

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Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
Db    3113 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 3054

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
Db    3053 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 2994

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
      2993 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 2934

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
Db    2933 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 2874

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
Db    2873 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 2814

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
Db    2813 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 2754

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
Db    2753 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 2694

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
Db    2693 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 2634

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
Db    2633 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 2574

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db    2573 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 2514

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
Db    2513 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 2454

Qy     221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
Db    2453 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 2394

Qy     241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
Db    2393 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 2334

Qy     261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
Db    2333 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 2274

Qy     281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
Db    2273 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 2214

Qy     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
Db    2213 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 2154

Qy     321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
Db    2153 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 2094

Qy     341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
Db    2093 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 2034

Qy     361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
Db    2033 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1974

Qy     381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
Db    1973 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1914

Qy     401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
Db    1913 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1854

Qy     421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
Db    1853 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1794

Qy     441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
Db    1793 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1734

Qy     461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
Db    1733 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1674

Qy     481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db    1673 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1614

Qy     501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
Db    1613 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1554

Qy     521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
Db    1553 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1494

Qy     541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
Db    1493 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1434

Qy     561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
Db    1433 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1374

Qy     581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
Db    1373 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1314

Qy     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
Db    1313 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1254

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
Db    1253 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1194

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
Db    1193 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1134

Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
Db    1133 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 1074

Qy     681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 1014

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 954

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 894

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 834

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 774

Qy    781 Lys 781
          |||
      773 AAA 771

RESULT 10
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1

Alignment Scores:
Pred. No.:              0              Length:        2994
Score:                  4014.00        Matches:       780
Percent Similarity:     100.00%        Conservative:  1
Best Local Similarity:  99.87%         Mismatches:    0
Query Match:            99.93%         Indels:        0
DB:                     5              Gaps:          0

US-09-026-459A-37 (1-781) x PCT-US94-10357-1 (1-2994)

Qy      1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy     21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy    101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy    121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599
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Qy     341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy     361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy     381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy     401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy     421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy     441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy     461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy     481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy     501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy     521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy     541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy     561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy     581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy     681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy     701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy     721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
           |||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCAGTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy     741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy     781 Lys 781
           |||
Db    2920 AAA 2922

RESULT 11
US-08-328-673A-7
; Sequence 7, Application US/08328673A
; Patent No. 6210939
;   GENERAL INFORMATION:
;        APPLICANT: Gregory, Richard J.
;                   Wills, Ken N.
;                   Maneval, Daniel C.
;        TITLE OF INVENTION: Recombinant Adenoviral Vector and
;                            Methods of Use
;        NUMBER OF SEQUENCES: 9
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/328,673A
;             FILING DATE: 25-Oct-1994
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/142,669
;             FILING DATE: 25-OCT-1993
;             APPLICATION NUMBER: US 08/233,669
;             FILING DATE: 26-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Smith, Timothy S.
;             REGISTRATION NUMBER: 35,367
;             REFERENCE/DOCKET NUMBER: 016930-000920US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2995 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  139..2925
;             OTHER INFORMATION:  /product= "RB"
;             /note= "retinoblastoma tumor suppressor"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-328-673A-7
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Alignment Scores:
Pred. No.:                0          Length:          2995
Score:                    4007.00    Matches:         780
Percent Similarity:       99.87%     Conservative:    0
Best Local Similarity:    99.87%     Mismatches:      1
Query Match:              99.75%     Indels:          0
DB:                       4          Gaps:            0

US-09-026-459A-37 (1-781) x US-08-328-673A-7 (1-2995)

Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg  20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer  40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle  80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
           ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCTTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy     341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy     361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy     381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy     401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy     421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy     441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy     461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy     481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy     501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy     521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy     541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy     561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy     581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619
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Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    781 Lys 781
          |||
Db   2920 AAA 2922

RESULT 12
US-07-708-962-1
; Sequence 1, Application US/07708962
; Patent No. 5262321
;  GENERAL INFORMATION:
;    APPLICANT:  Livingston, David M.
;    APPLICANT:  Ewen, Mark E.
;    TITLE OF INVENTION:  Tumor Suppressor
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Choate, Hall & Stewart
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/708,962
;      FILING DATE:  19910531
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kennedy, Bill
;      REGISTRATION NUMBER:  33,407
;      REFERENCE/DOCKET NUMBER:  DFCI 209
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-5020
;      TELEFAX:  (617) 227-7566
;      TELEX:  289374
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2808 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-708-962-1

Alignment Scores:
Pred. No.:              5.1e-76       Length:        2808
Score:                  768.00        Matches:       247
Percent Similarity:     38.27%        Conservative:  130

Best Local Similarity:  25.08%        Mismatches:    268
Query Match:            19.12%        Indels:        340
DB:                     1             Gaps:          30

US-09-026-459A-37 (1-781) x US-07-708-962-1 (1-2808)

Qy      4 LeuLeuLysLysTyrAspValLeuPheAla---LeuPheSer----------------- 16
          :::   ||||||||||:::   :::|||      :::|||
Db      4 ATATTCAAAAAATATGAGCCAATTTTTTTAGATATATTTCAAAATCCATATGAAGAACCA 63

Qy     17 ---LysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSer 35
            ||||||  |||                    ::::::          |||
Db     64 CCAAAGTTACCACGA-------------------AGCCGGAAGCAGAGGAGGATTCCT 102

Qy     36 ThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLys 55
              :::         :::          |||      |||:::      |||
Db    103 TGCAGTGTTAAGGAT------CTGTTTAATTTCTGTTGGACACTTTTTGTTTATACTAAG 156

Qy     56 GlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysVal 75
          |||           :::   ||||||||||||   |||:::   |||:::||||||
Db    157 GGTAATTTTCGGATGATTGGGGATGACTTAGTAAACTCTTATCATTTACTTCTATGCTGC 216

Qy     76 LeuAspTyrPheIleLys---------------------------------LeuSerPro 84
          ||||||                                           |||:::|||
Db    217 TTGGATCTGATTTTTGCCAATGCGATTATGTGCCCAAATAGACAAGACTTGCTAAATCCA 276

Qy     85 ProMetLeu---LeuLysGluProTyrLysThrAlaValIleProIleAsnGlySerPro 103
                  |||         :::   ||||||            :::      |||
Db    277 TCATTTAAAGGTTTACCATCTGATTTTCATACTGCTGACTTTACGGCTTCTGAAGAGCCA 336

Qy    104 ArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAsp 123

Db    337 CCCTGC---------------------------------------------------- 342

Qy    124 ThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsn 143
              ||||||   |||||||||:::   |||:::    :::   |||   |||
Db    343 ------ATCATTGCTGTACTGTGTGAACTGCATGATGGACTTCTCGTAGAAGCAAAAGGA 396

Qy    144 Val---------TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
          :::         |||||||||   :::|||      :::            ::::::
Db    397 ATAAAGGAGCACTACTTTAAGCCATATATTTCAAAACTCTTTGACAGGAAGATATTAAAA 456

Qy    161 SerAsnGlyLeuProGluValGluAsn---------------------LeuSerLysArg 173
                |||   ::::::   :::                        ::::::|||
Db    457 GGAGAATGCCTCCTGGACCTTTCAAGTTTTACTGATAATAGCAAAGCAGTGAATAAGGAG 516

Qy    174 TyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAsp 193
          |||||||||      |||          |||   |||   |||:::||||||
Db    517 TATGAAGAGTATGTTCTAACTGTTGGTGATTTTGATGAGAGGATCTTTTTG--------- 567

Qy    194 LysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArgLys--- 212
                                    |||:::   |||          ||||||||||||
Db    568 -----------------GGAGCAGACGCAGAAGAGGAAATTGGAACACCTCGAAAGTTC 609

Qy    213 -----------------SerAsnLeuAspGluGluValAsnVal---------IlePro 223
                                    |||      :::   ||||||         :::
Db    610 ACTCGTGACACCCCATTAGGGAAACTGACAGCACAGGCTAATGTGGAGTATAACCTTCAA 669

Qy    224 ProHis------------------------------------------------------ 225
          |||
Db    670 CAGCACTTTGAAAAAAAAAGGTCATTTGCACCTTCTACCCCACTGACCGGACGGAGATAT 729

Qy    226 ----------------------ThrProValArgThrValMetAsnThrIleGlnGln 237
                                  |||||||||   :::          ::::::   :::
Db    730 TTACGAGAAAAAGAAGCAGTCATTACTCCTGTTGCATCAGCCACCCAAAGTGTGAGCCGG 789

Qy    238 LeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPhe 257
          |||      |||:::            :::   ||||||:::   ||||||:::   |||
Db    790 TTACAGAGTATTGTGGCTGGTCTGAAAAATGCACCAAGTGACCAACTTATAAATATTTTT 849

Qy    258 AsnAsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyr 277
            ::::||      ||||||   |||:::|||::|||   :::|||   ||||||
Db    850 GAATCTTGTGTGCGTAATCCTGTGGAAAACATTATGAAAATACTAAAAGGAATAGGAGAG 909
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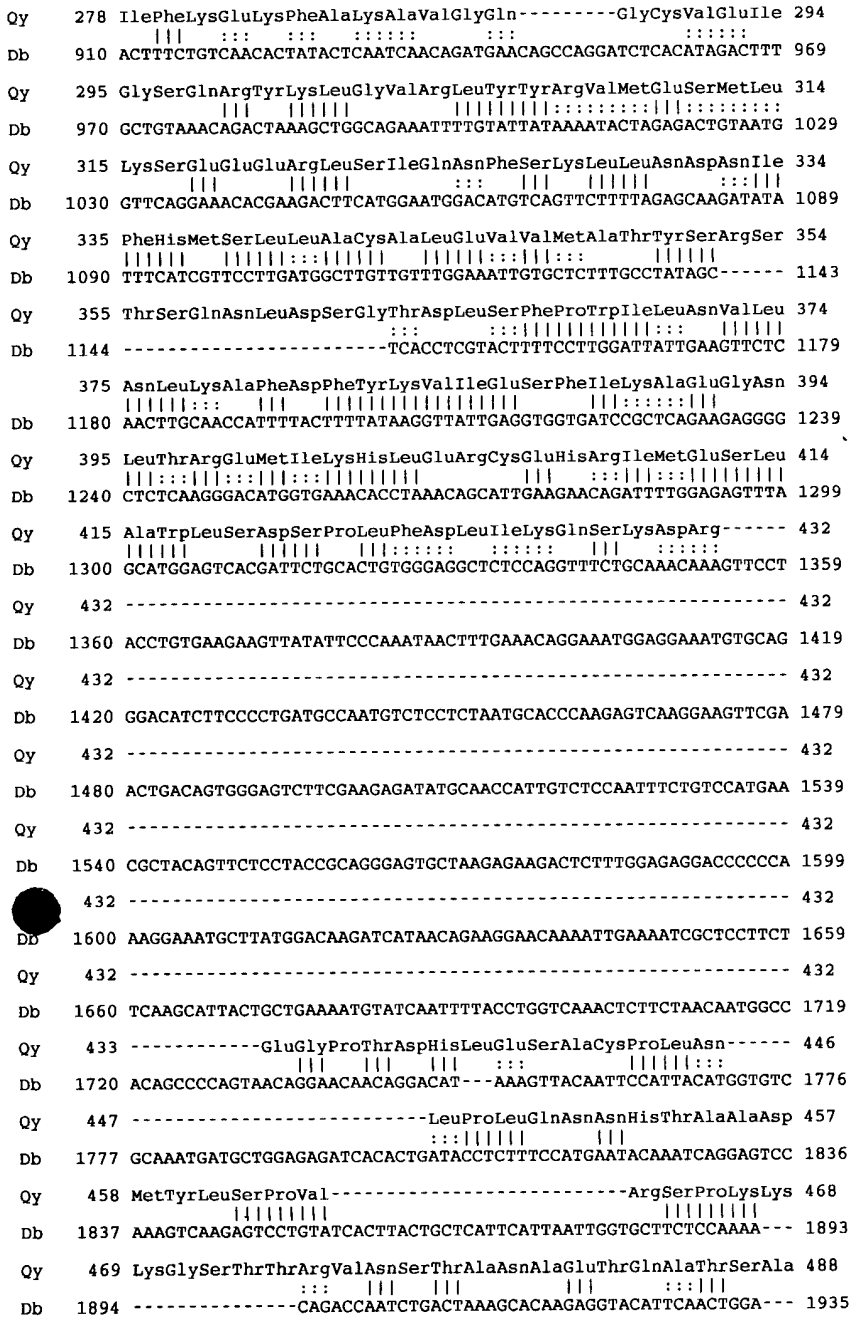

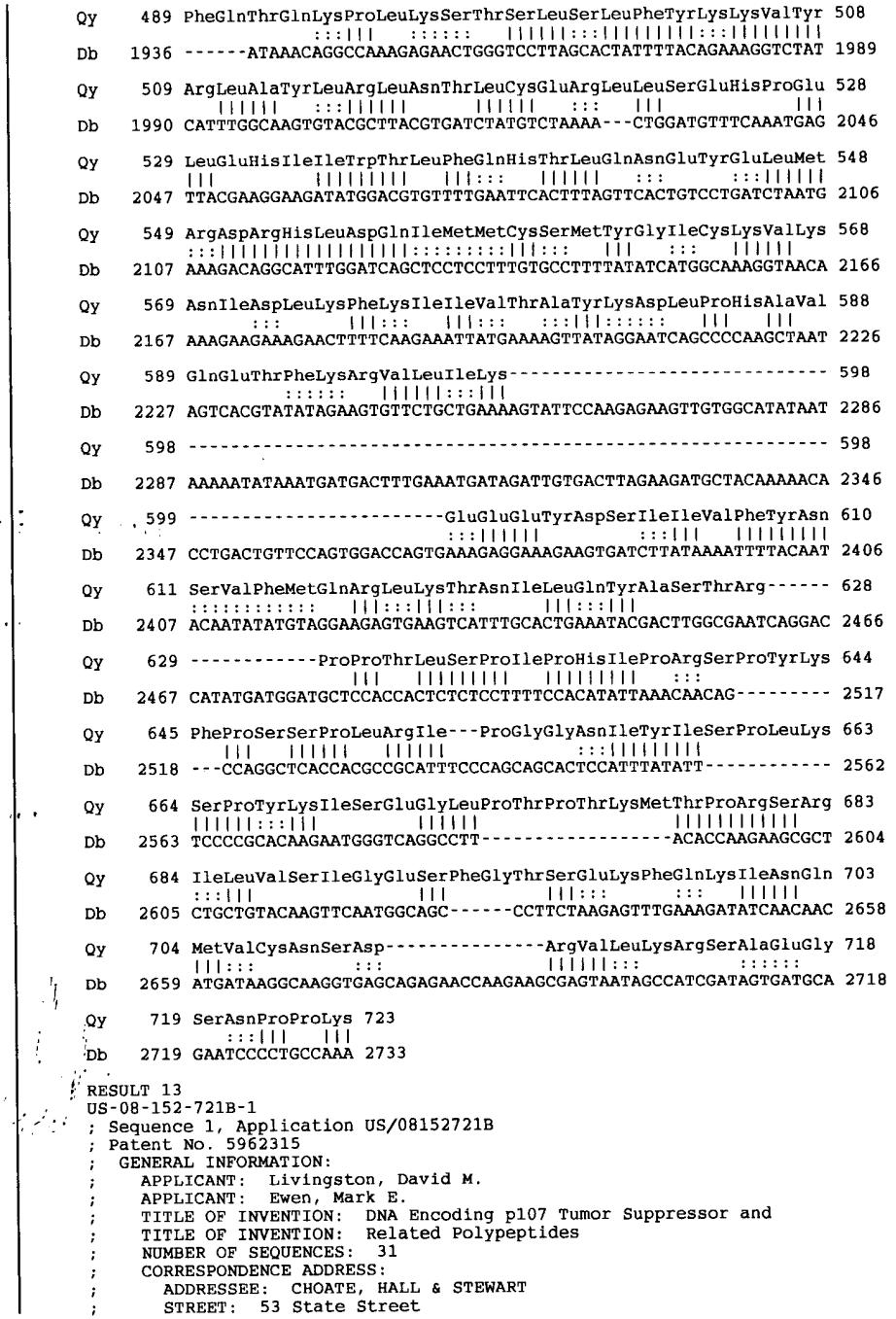

RESULT 13
US-08-152-721B-1
; Sequence 1, Application US/08152721B
; Patent No. 5962315
; GENERAL INFORMATION:
; APPLICANT: Livingston, David M.
; APPLICANT: Ewen, Mark E.
; TITLE OF INVENTION: DNA Encoding p107 Tumor Suppressor and
; TITLE OF INVENTION: Related Polypeptides
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street

```
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2891
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/152,721B
;      FILING DATE:  15-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pasternack Esq., Sam
;      REGISTRATION NUMBER:  29,576
;      REFERENCE/DOCKET NUMBER:  181411-011DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-5000
;      TELEFAX:  (617) 248-4000
;    INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2808 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  cDNA encoding p107
US-08-152-721B-1

Alignment Scores:
Pred. No.:                1.87e-75      Length:          2808
Score:                    763.00        Matches:         246
Percent Similarity:       38.17%        Conservative:    130
Best Local Similarity:    24.97%        Mismatches:      269
Query Match:              18.99%        Indels:          340
DB:                       2             Gaps:            30

US-09-026-459A-37 (1-781) x US-08-152-721B-1 (1-2808)

Qy       4 LeuLeuLysLysTyrAspValLeuPheAla---LeuPheSer------------------ 16
           :::   ||||||||::   :::|||      :::|||
Db       4 ATATTCAAAAAATATGAGCCAATTTTTTTAGATATATTTCAAAATCCATATGAAGAACCA 63

Qy      17 ---LysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSer 35
              ||||||   |||                ::::::          |||
Db      64 CCAAAGTTACCACGA--------------------AGCCGGAAGCAGAGGAGGATTCCT 102

Qy      36 ThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLys 55
             :::          :::          |||      |||:::      |||
Db     103 TGCAGTGTTAAGGAT------CTGTTTAATTTCTGTTGGACACTTTTTGTTTATACTAAG 156

Qy      56 GlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysVal 75
           |||           :::   ||||||||||||   |||:::   |||:::||||||
Db     157 GGTAATTTTCGGATGATTGGGGATGACTTAGTAAACTCTTATCATTTACTTCTATGCTGC 216

Qy      76 LeuAspTyrPheIleLys------------------------------LeuSerPro 84
           ||||||                                          |||:::|||
Db     217 TTGGATCTGATTTTTGCCAATGCGATTATGTGCCCAAATAGACAAGACTTGCTAAATCCA 276

Qy      85 ProMetLeu---LeuLysGluProTyrLysThrAlaValIleProIleAsnGlySerPro 103
                  |||        :::   ||||||            :::      |||
Db     277 TCATTTAAAGGTTTACCATCTGATTTTCATACTGCTGACTTTACGGCTTCTGAAGAGCCA 336

Qy     104 ArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAsp 123

Db     337 CCCTGC---------------------------------------------------- 342

Qy     124 ThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsn 143
              ||||||   |||||||||:::   |||:::      :::   |||   |||

Db     343 ------ATCATTGCTGTACTGTGTGAACTGCATGATGGACTTCTCGTAGAAGCAAAAGGA 396

Qy     144 Val---------TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
           :::         |||||||||   :::|||      :::            ::::::
Db     397 ATAAAGGAGCACTACTTTAAGCCATATATTTCAAAACTCTTTGACAGGAAGATATTAAAA 456

Qy     161 SerAsnGlyLeuProGluValGluAsn--------------------LeuSerLysArg 173
                  |||   ::::::   :::                     :::::|||
Db     457 GGAGAATGCCTCCTGGACCTTTCAAGTTTTACTGATAATAGCAAAGCAGTGAATAAGGAG 516

Qy     174 TyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAsp 193
           |||||||||      |||      |||   |||   |||:::|||||
Db     517 TATGAAGAGTATGTTCTAACTGTTGGTGATTTTGATGAGAGGATCTTTTTG--------- 567

Qy     194 LysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArgLys--- 212
                                       |||:::   |||         ||||||||||
Db     568 ------------------GGAGCAGACGCAGAAGAGGAAATTGGAACACCTCGAAAGTTC 609

Qy     213 ------------------SerAsnLeuAspGluGluValAsnVal---------IlePro 223
                                       |||      :::   ||||||         :::
Db     610 ACTCGTGACACCCCATTAGGGAAACTGACAGCACAGGCTAATGTGGAGTATAACCTTCAA 669

Qy     224 ProHis------------------------------------------------------ 225
           |||
Db     670 CAGCACTTTGAAAAAAAAAGGTCATTTGCACCTTCTACCCCACTGACCGGACGGAGATAT 729

Qy     226 ------------------------ThrProValArgThrValMetAsnThrIleGlnGln 237
                                       |||||||||   :::         ::::::   :::
Db     730 TTACGAGAAAAAGAAGCAGTCATTACTCCTGTTGCATCAGCCACCCAAAGTGTGAGCCGG 789

Qy     238 LeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPhe 257
           |||      |||:::           :::   ||||||:::   |||||||:::   |||
Db     790 TTACAGAGTATTGTGGCTGGTCTGAAAAATGCACCAAGTGACCAACTTATAAATATTTTT 849

Qy     258 AsnAsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyr 277
              :::|||      ||||||   |||:::|||:::|||   :::|||   ||||||
Db     850 GAATCTTGTGTGCGTAATCCTGTGGAAAACATTATGAAAATACTAAAAGGAATAGGAGAG 909

Qy     278 IlePheLysGluLysPheAlaLysAlaValGlyGln---------GlyCysValGluIle 294
              |||   :::   :::   ::::::          :::                ::::::
Db     910 ACTTTCTGTCAACACTATACTCAATCAACAGATGAACAGCCAGGATCTCACATAGACTTT 969

Qy     295 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeu 314
                 |||   ||||||          |||||||||:::::::::|||:::::::::
Db     970 GCTGTAAACAGACTAAAGCTGGCAGAAATTTTGTATTATAAAATACTAGAGACTGTAATG 1029

Qy     315 LysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 334
                 |||      ||||||          :::   |||   ||||||      :::|||
Db    1030 GTTCAGGAAACACGAAGACTTCATGGAATGGACATGTCAGTTCTTTTAGAGCAAGATATA 1089

Qy     335 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSer 354
           ||||||   ||||||:::||||||   ||||||:::|||:::      ||||||
Db    1090 TTTCATCGTTCCTTGATGGCTTGTTGTTTGGAAATTGTGCTCTTTGCCTATAGC------ 1143

Qy     355 ThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeu 374
                                       :::      :::|||||||||||:::   ||||||
Db    1144 ------------------------TCACCTCGTACTTTTCCTTGGATTATTGAAGTTCTC 1179

Qy     375 AsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 394
           |||||||::   |||   ||||||||||||||||||      |||:::::::|||
Db    1180 AACTTGCAACCATTTTACTTTTATAAGGTTATTGAGGTGGTGATCCGCTCAGAAGAGGGG 1239

Qy     395 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeu 414
           |||:::|||:::|||:::||||||||||          |||   :::|||:::||||||||
Db    1240 CTCTCAAGGGACATGGTGAAACACCTAAACAGCATTGAAGAACAGATTTTGGAGAGTTTA 1299

Qy     415 AlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArg------ 432
           ||||||      ||||||   |||::::::   ::::::   |||   ::::::
Db    1300 GCATGGAGTCACGATTCTGCACTGTGGGAGGCTCTCCAGGTTTCTGCAAACAAAGTTCCT 1359

Qy     432 ------------------------------------------------------------ 432

Db    1360 ACCTGTGAAGAAGTTATATTCCCAAATAACTTTGAAACAGGAAATGGAGGAAATGTGCAG 1419
```

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Qy    432 ------------------------------------------------------------ 432
Db   1420 GGACATCTTCCCCTGATGCCAATGTCTCCTCTAATGCACCCAAGAGTCAAGGAAGTTCGA 1479
Qy    432 ------------------------------------------------------------ 432
Db   1480 ACTGACAGTGGGAGTCTTCGAAGAGATATGCAACCATTGTCTCCAATTTCTGTCCATGAA 1539
Qy    432 ------------------------------------------------------------ 432
Db   1540 CGCTACAGTTCTCCTACCGCAGGGAGTGCTAAGAGAAGACTCTTTGGAGAGGACCCCCCA 1599
Qy    432 ------------------------------------------------------------ 432
Db   1600 AAGGAAATGCTTATGGACAAGATCATAACAGAAGGAACAAAATTGAAAATCGCTCCTTCT 1659
Qy    432 ------------------------------------------------------------ 432
Db   1660 TCAAGCATTACTGCTGAAAATGTATCAATTTTACCTGGTCAAACTCTTCTAACAATGGCC 1719
Qy    433 ------------GluGlyProThrAspHisLeuGluSerAlaCysProLeuAsn------ 446
Db   1720 ACAGCCCCAGTAACAGGAACAACAGGACAT---AAAGTTACAATTCCATTACATGGTGTC 1776
Qy    447 --------------------------LeuProLeuGlnAsnAsnHisThrAlaAlaAsp 457
Db   1777 GCAAATGATGCTGGAGAGATCACACTGATACCTCTTTCCATGAATACAAATCAGGAGTCC 1836
Qy    458 MetTyrLeuSerProVal--------------------------ArgSerProLysLys 468
Db   1837 AAAGTCAAGAGTCCTGTATCACTTACTGCTCATTCATTAATTGGTGCTTCTCCAAAA--- 1893
Qy    469 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 488
Db   1894 --------------CAGACCAATCTGACTAAAGCACAAGAGGTACATTCAACTGGA--- 1935
Qy    489 PheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyr 508
Db   1936 ------ATAAACAGGCCAAAGAGAACTGGGTCCTTAGCACTATTTTACAGAAAGGTCTAT 1989
Qy    509 ArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGlu 528
Db   1990 CATTTGGCAAGTGTACGCTTACGTGATCTATGTCTAAAA---CTGGATGTTTCAAATGAG 2046
Qy    529 LeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMet 548
Db   2047 TTACGAAGGAAGATATGGACGTGTTTTGAATTCACTTTAGTTCACTGTCCTGATCTAATG 2106
Qy    549 ArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLys 568
Db   2107 AAAGACAGGCATTTGGATCAGCTCCTCCTTTGTGCCTTTTATATCATGGCAAAGGTAACA 2166
Qy    569 AsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaVal 588
Db   2167 AAAGAAGAAAGAACTTTTCAAGAAATTATGAAAAGTTATAGGAATCAGCCCCAACGTAAT 2226
Qy    589 GlnGluThrPheLysArgValLeuIleLys---------------------------- 598
Db   2227 AGTCACGTATATAGAAGTGTTCTGCTGAAAAGTATTCCAAGAGAAGTTGTGGCATATAAT 2286
Qy    598 ------------------------------------------------------------ 598
Db   2287 AAAAATATAAATGATGACTTTGAAATGATAGATTGTGACTTAGAAGATGCTACAAAAACA 2346
Qy    599 ----------------------GluGluGluTyrAspSerIleIleValPheTyrAsn 610
Db   2347 CCTGACTGTTCCAGTGGACCAGTGAAAGAGGAAAGAAGTGATCTTATAAAATTTTACAAT 2406
Qy    611 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArg------ 628
Db   2407 ACAATATATGTAGGAAGAGTGAAGTCATTTGCACTGAAATACGACTTGGCGAATCAGGAC 2466

Qy    629 ------------ProProThrLeuSerProIleProHisIleProArgSerProTyrLys 644
Db   2467 CATATGATGGATGCTCCACCACTCTCTCCTTTTCCACATATTAAACAACAG--------- 2517
Qy    645 PheProSerSerProLeuArgIle---ProGlyGlyAsnIleTyrIleSerProLeuLys 663
Db   2518 ---CCAGGCTCACCACGCCGCATTTCCCAGCAGCACTCCATTTATATT------------ 2562
Qy    664 SerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 683
Db   2563 TCCCCGCACAAGAATGGGTCAGGCCTT-----------------ACACCAAGAAGCGCT 2604
Qy    684 IleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGln 703
Db   2605 CTGCTGTACAAGTTCAATGGCAGC------CCTTCTAAGAGTTTGAAAGATATCAACAAC 2658
Qy    704 MetValCysAsnSerAsp--------------ArgValLeuLysArgSerAlaGluGly 718
Db   2659 ATGATAAGGCAAGGTGAGCAGAGAACCAAGAAGCGAGTAATAGCCATCGATAGTGATGCA 2718
Qy    719 SerAsnProProLys 723
Db   2719 GAATCCCCTGCCAAA 2733
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RESULT 14
US-08-832-883-1
; Sequence 1, Application US/08832883
; Patent No. 5807681
; GENERAL INFORMATION:
; APPLICANT: Giordano, Antonio
; APPLICANT: Baldi, Alphonso
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
; TITLE OF INVENTION: OF CANCER
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
; STREET: Suite 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,883
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-13 US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4853 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 70..3489
US-08-832-883-1

Alignment Scores:

Pred. No.:	3.08e-71	Length:	4853
Score:	729.50	Matches:	252
Percent Similarity:	38.33%	Conservative:	147

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Best Local Similarity:  24.21%        Mismatches:    305
Query Match:            18.16%        Indels:        337
DB:                     1             Gaps:          32

US-09-026-459A-37 (1-781) x US-08-832-883-1 (1-4853)

Qy       3 ArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArgThrCys  22
Db     520 AGATTAGAAAGAAACTTCACTGTTTCTGCTGTAATTTTTAAGAAATATGAACCCATTTTT  579

Qy      23 GluLeuIleTyrLeu-----------ThrGlnProSerSerSerIleSerThrGlu---  37
Db     580 CAGGACATCTTTAAATACCCTCAAGAGGAGCAACCTCGTCAGCAGCGAGGAAGGAAACAG  639

Qy      38 ------------IleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeu  53
Db     640 CGGCGACAGCCCTGTACTGTGTCTGAAATTTTCCATTTTTGTTGGGTGCTTTTTATATAT  699

Qy      54 AlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMetLeu  73
Db     700 GCAAAAGGTAATTTCCCCATGATTAGTGATGATTTGGTCAATTCTTATCACCTGCTGCTG  759

Qy      74 CysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLys  93
Db     760 TGTGCTTTGGACTTAGTT----------------------------------TATGGA  783

Qy      94 ThrAlaValIleProIleAsnGly------------SerProArgThrProArgArgGly 109
Db     784 AATGCACTTCAGTGTTCTAATCGTAAAGAACTTGTGAACCCTAATTTTAAAGGCTTATCT  843

Qy     110 GlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluVal 129
Db     844 GAAGATTTTCATGCTAAAGATTCTAAACCTTCCTCTGACCCCCCTTGTATCATTGAGAAA  903

Qy     130 LeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal---------TyrPhe 146
Db     904 CTGTGTTCCTTACATGATGGCCTAGTTTTGGAAGCAAAGGGGATAAAGGAACATTTCTGG  963

Qy     147 LysAsnPheIleProPheMet--------------------------------AsnSer 155
Db     964 AAACCCTATATTAGGAAACTTTATGAAAAAAAGCTCCTTAAGGGAAAAGAAGAAAATCTC 1023

Qy     156 LeuGlyLeuValThrSerAsnGlyLeuProGlu---ValGluAsnLeuSerLysArgTyr 174
Db    1024 ACTGGGTTTCTAGAACCTGGGAACTTTGGAGAGAGTTTTAAAGCCATCAATAAGGCCTAT 1083

Qy     175 GluGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAsp---  193
      1084 GAGGAGTATGTTTTATCTGTTGGGAATTTAGATGAGCGGATATTTCTTGGAGAGGATGCT 1143

Qy     193 ------------------------------------------------------------  193
Db    1144 GAGGAGGAAATTGGGACTCTCTCAAGGTGTCTGAACGCTGGTTCAGGAACAGAGACTGCT 1203

Qy     194 LysThrLeuGlnThrAspSerIle------AspSerPheGluThrGlnArgThrProArg  211
Db    1204 GAAAGGGTGCAGATGAAAAACATCTTACAGCAGCATTTTGACAAGTCCAAAGCACTTAGA 1263

Qy     212 LysSerAsnLeuAspGluGluValAsnValIle------------ProProHisThrPro  227
Db    1264 ATCTCCACACCACTAACTGGTGTTAGGTACATTAAGGAGAATAGCCCTTGTGTGACTCCA 1323

Qy     228 ValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAsp  247
Db    1324 GTTTCTACAGCTACGCATAGCTTGAGTCGTCTTCACACCATGCTGACAGGCCTCAGGAAT 1383

Qy     248 GlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSer  267
Db    1384 GCACCAAGTGAGAAACTGGAACAGATTCTCAGGACATGTTCCAGAGATCCAACCCAGGCT 1443

Qy     268 IleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla------Lys  285
Db    1444 ATTGCTAACAGACTGAAAGAAATGTTTGAAATATATTCTCAGCATTTCCAGCCAGACGAG 1503

Qy     286 AlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeu 305
Db    1504 GATTTCAGTAATTGTGCTAAAGAAATTGCCAGCAAACATTTTCGTTTTGCGGAGATGCTT 1563

Qy     306 TyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsn  325
Db    1564 TACTATAAAGTATTAGAATCTGTTATTGAGCAGGAACAAAAAAGACTAGGAGACATGGAT 1623

Qy     326 PheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGlu  345
Db    1624 TTATCTGGTATTCTGGAACAAGATGCATTCCACAGATCTCTCTTGGCCTGCTGCCTTGAG 1683

Qy     346 ValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu  365
Db    1684 GTCGTC------ACTTTTTCTTATAAGCCTCCTGGGAAT---------------------- 1716

Qy     366 SerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIle  385
Db    1717 ---TTTCCATTTATTACTGAAATATTTGATGTGCCTCTTTATCATTTTTATAAGGTGATA 1773

Qy     386 GluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArg  405
Db    1774 GAAGTATTCATTAGAGCAGAAGATGGCCTTTGTAGAGAGGTGGTAAAACACCTTAATCAG 1833

Qy     406 CysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeu  425
Db    1834 ATTGAAGAACAGATCTTAGATCATTTGGCATGGAAACCAGAGTCTCCACTCTGGGAAAAA 1893

Qy     426 IleLysGlnSerLysAspArgGluGly------------------ProThrAspHisLeu  439
Db    1894 ATTAGAGACAATGAAAACAGAGTTCCTACATGTGAAGAGGTCATGCCACCTCAGAACCTG 1953

Qy     440 GluSerAla---------CysProLeuAsnLeuProLeuGlnAsnAsnHis--------- 453
Db    1954 GAAAGGGCAGATGAAATTTGCATTGCTGGCTCCCCTTTGACTCCCAGAAGGGTGACTGAA 2013

Qy     454 ------------------------------------------------ThrAlaAlaAsp 457
Db    2014 GTTCGTGCTGATACTGGAGGACTTGGAAGGAGCATAACATCTCCAACCACATTATACGAT 2073

Qy     458 MetTyrLeuSerProValArgSerProLysLysLys------------------------ 469
Db    2074 AGGTACAGCTCCCCACCAGCCAGCACTACCAGAAGGCGGCTATTTGTTGAGAATGATAGC 2133

Qy     469 ------------------------------------------------------------  469
Db    2134 CCCTCTGATGGAGGGACGCCTGGGCGCATGCCCCCACAGCCCCTAGTCAATGCTGTCCCT 2193

Qy     470 ---------------GlySerThrThrArgValAsnSer---------------------- 477
Db    2194 GTGCAGAATGTATCTGGGGAGACTGTTTCTGTCACACCAGTTCCTGGACAGACTTTGGTC 2253

Qy     478 ---------------------ThrAlaAsn----------------------------- 480
Db    2254 ACCATGGCAACCGCCACTGTCACAGCCAACAATGGGCAAACGGTAACCATTCCTGTGCAA 2313

Qy     481 ------------------------------------------------------------Ala 481
Db    2314 GGTATTGCCAATGAAAATGGAGGGATAACATTCTTCCCTGTCCAAGTCAATGTTGGGGGG 2373

Qy     482 GluThrGlnAla---ThrSerAlaPheGln------------------------------ 490
Db    2374 CAGGCACAAGCTGTGACAGGCTCCATCCAGCCCCTCAGTGCTCAGGCCCTGGCTGGAAGT 2433

Qy     490 ------------------------------------------------------------  490
Db    2434 CTGAGCTCTCAACAGGTGACAGGAACAACTTTGCAAGTCCCTGGTCAAGTGGCCATTCAA 2493

Qy     491 ------------------------------------------------------ThrGln 492
Db    2494 CAGATTTCCCCAGGTGGCCAACAGCAGAAGCAAGGCCAGTCTGTAACCAGCAGTAGTAAT 2553
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Qy     493 LysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyr 512
           :::|||   |||::::::|||||||||||||||||:::::|||||||||   ||||||
Db    2554 AGACCCAGGAAGACCAGCTCTTTATCGCTTTTCTTTAGAAAGGTATACCATTTAGCAGCT 2613

Qy     513 LeuArgLeuAsnThrLeuCysGluArgLeu---LeuSerGluHisProGluLeuGluHis 531
           :::|||||||      ||||||   :::|||   :::|||:::      |||||||
Db    2614 GTCCGCCTTCGGGATCTCTGTGCCAAACTAGATATTTCAGAT------GAATTGAGGAAA 2667

Qy     532 IleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArg 551
           |||||||||  |||:::  ::::::                |||||||||  ||||||
Db    2668 AAAATCTGGACCTGCTTTGAATTCTCCATAATTCAGTGTCCTGAACTTATGATGGACAGA 2727

Qy     552 HisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAsp 571
           ||||||||||||:::::||||||:::::|||   :::   ||||||        |||
Db    2728 CATCTGGACCAGTTATTAATGTGTGCCATTTATGTGATGGCAAAGGTCACAAAAGAAGAT 2787

Qy     572 LeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluThr 591
           |||:::  |||:::      |||:::      |||   |||      :::
Db    2788 AAGTCCTTCCAGAACATTATGCGTTGTTATAGGACTCAGCCGCAGGCCCGGAGCCAGGTG 2847

       592 PheLysArgValLeuIleLys---------------------------------------- 598
           ::::::  ||||||||||||
      2848 TATAGAAGTGTTTTGATAAAAGGGAAAAGAAAAAGAAGAAATTCTGGCAGCAGTGATAGC 2907

Qy     598 ---------------------------------------------------------- 598

Db    2908 AGAAGCCATCAGAATTCTCCAACAGAACTAAACAAAGATAGAACCAGTAGAGACTCCAGT 2967

Qy     598 ---------------------------------------------------------- 598

Db    2968 CCAGTTATGAGGTCAAGCAGCACCTTGCCAGTTCCACAGCCCAGCAGTGCTCCTCCCACA 3027

Qy     599 ----------------------------------GluGluGluTyrAspSerIleIle 606
                                               |||||||||      :::|||
Db    3028 CCTACTCGCCTCACAGGTGCCAACAGTGACATGGAAGAAGAGGAGAGGGCAGACCTCATT 3087

Qy     607 ValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyr------ 624
           |||||||||:::::::::::::::::::::::::||||||      :::::::|||
Db    3088 CAGTTCTACAACAACATCTACATCAAACAGATTAAGACATTTGCCATGAAGTACTCACAG 3147

Qy     625 AlaSerThrArgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 644
           |||:::         |||   |||||||||   |||   :::
Db    3148 GCAAATATGGATGCTCCTCCACTCTCTCCCTATCCATTTGTAAGA-------------- 3192

Qy     645 PheProSerSerProLeuArgIle---------ProGlyGlyAsnIleTyrIleSerPro 661
                 ||||||   ||||||                    :::|||||||||||||
Db    3193 ---ACAGGCTCCCCTCGCCGAATACAGTTGTCTCAAAATCATCCTGTCTACATTTCCCCA 3249

Qy     662 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArg 681
           |||:::                                |||   ::::::|||||||
Db    3250 CATAAAAAT----------------------------GAAACAATGCTTTCTCCTCGA 3279

Qy     682 SerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIle 701
             :::|||                  |||         |||::::::   ::::::|||
Db    3280 GAAAAGATTTTCTATTACTTCAGCAACAGT------CCTTCAAAGAGACTGAGAGAAATT 3333

Qy     702 AsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnPro 721
           |||   |||:::                        |||:::   |||
Db    3334 AATAGTATGATA----------------------CGCACAGGAGAA------------ 3357

Qy     722 ProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGlySer 741
               |||   ||||||          :::|||         |||:::
Db    3358 ---ACTCCTACTAAAAAGAGAGGAATTCTTTTGGAAGATGGAAGTGAATCACCTGCAAAA 3414

Qy     742 LysHisLeuPro---GlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
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RESULT 15

US-08-832-877-1
; Sequence 1, Application US/08832877
; Patent No. 5840506
;  GENERAL INFORMATION:
;    APPLICANT:  Giordano, Antonio
;    TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
;    TITLE OF INVENTION:  CANCER
;    NUMBER OF SEQUENCES:  116
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
;      STREET:  Suite 1800 Two Penn Center Plaza
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,877
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  8321-13 US2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4853 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  70..3489
US-08-832-877-1

Alignment Scores:
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Score:                    729.50          Matches:         252
Percent Similarity:       38.33%          Conservative:    147
Best Local Similarity:    24.21%          Mismatches:      305
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US-09-026-459A-37 (1-781) x US-08-832-877-1 (1-4853)

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Db     520 AGATTAGAAAGAAACTTCACTGTTTCTGCTGTAATTTTTAAGAAATATGAACCCATTTTT 579

Qy      23 GluLeuIleTyrLeu-----------ThrGlnProSerSerSerIleSerThrGlu--- 37
           :::   |||:::                  ||||||                  :::
Db     580 CAGGACATCTTTAAATACCCTCAAGAGGAGCAACCTCGTCAGCAGCGAGGAAGGAAACAG 639

Qy      38 -----------IleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeu 53
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Db     640 CGGCGACAGCCCTGTACTGTGTCTGAAATTTTCCATTTTTGTTGGGTGCTTTTTATATAT 699

Qy      54 AlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMetLeu 73
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Db     700 GCAAAAGGTAATTTCCCCATGATTAGTGATGATTTGGTCAATTCTTATCACCTGCTGCTG 759

Qy      74 CysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLys 93
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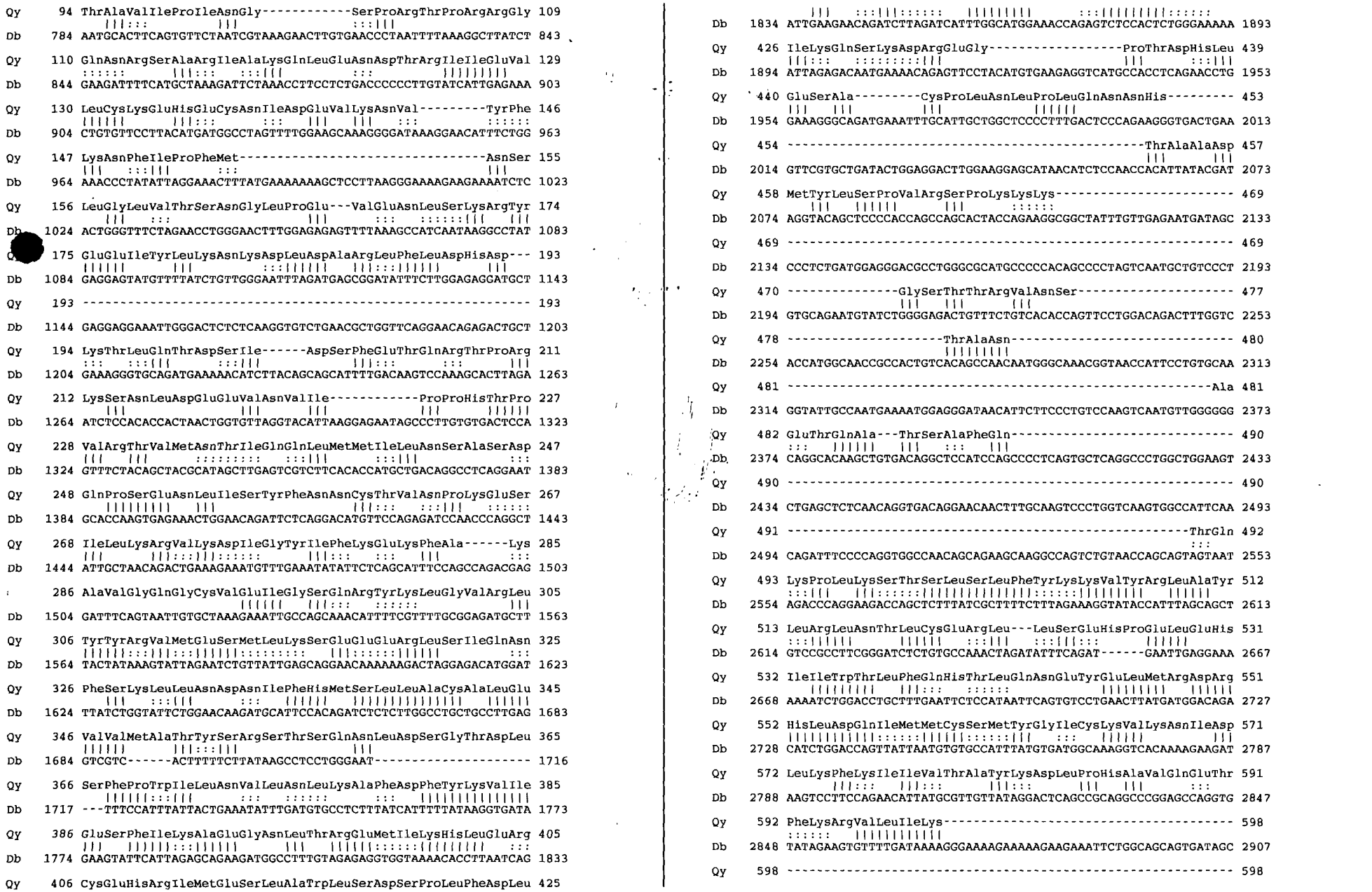

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Db   3028 CCTACTCGCCTCACAGGTGCCAACAGTGACATGGAAGAAGAGGAGAGGGGAGACCTCATT 3087

Qy    607 ValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyr------ 624
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Db   3088 CAGTTCTACAACAACATCTACATCAAACAGATTAAGACATTTGCCATGAAGTACTCACAG 3147

Qy    625 AlaSerThrArgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 644
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      3193 ---ACAGGCTCCCCTCGCCGAATACAGTTGTCTCAAAATCATCCTGTCTACATTTCCCCA 3249

       662 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArg 681
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Db   3250 CATAAAAAT----------------------------GAAACAATGCTTTCTCCTCGA 3279

Qy    682 SerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIle 701
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Qy    742 LysHisLeuPro---GlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
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Db   3415 AGAATTTGCCCAGAAAATCATTCTGCCTTATTACGCCGTCTCCAAGATGTAGCTAATGAC 3474

Qy    761 Arg 761
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Job time : 114.428 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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Perfect score: 3113
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

[redacted]mum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	3105.4	99.8	3232	1	US-08-038-760-2	Sequence 2, Appli
	3	3105.4	99.8	3232	2	US-08-470-091-1	Sequence 1, Appli
	[redacted]	3105.4	99.8	3232	2	US-08-470-091-2	Sequence 2, Appli
	[redacted]	2415	77.6	2994	1	US-08-204-329-2	Sequence 2, Appli
	6	2415	77.6	2994	2	US-08-482-627-4	Sequence 4, Appli
	7	2415	77.6	2994	3	US-08-801-092-3	Sequence 3, Appli
	8	2415	77.6	2994	4	US-09-315-113-3	Sequence 3, Appli
	9	2413.4	77.5	2994	5	PCT-US94-10357-1	Sequence 1, Appli
	10	2412	77.5	2995	2	US-08-959-638-7	Sequence 7, Appli
	11	2410.4	77.4	2995	4	US-08-328-673A-7	Sequence 7, Appli
	12	68.8	2.2	2808	1	US-07-708-962-1	Sequence 1, Appli
	13	68.2	2.2	3249	1	US-08-106-493A-1	Sequence 1, Appli
	14	68.2	2.2	3249	1	US-08-429-264-1	Sequence 1, Appli
	15	68.2	2.2	4853	1	US-08-832-883-1	Sequence 1, Appli
	16	68.2	2.2	4853	2	US-08-832-877-1	Sequence 1, Appli
	17	65.6	2.1	2808	2	US-08-152-721B-1	Sequence 1, Appli
c	18	59	1.9	7218	1	US-08-232-463-14	Sequence 14, Appl
	19	51	1.6	3747	4	US-09-213-293D-2	Sequence 2, Appli
	20	44.6	1.4	1803	4	US-09-134-001C-799	Sequence 799, App
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c	22	44.4	1.4	20674	4	US-09-641-638-651	Sequence 651, App
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	27	43.2	1.4	509	4	US-09-439-313-202	Sequence 202, App
	28	43.2	1.4	509	4	US-09-352-616A-202	Sequence 202, App
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	31	42.8	1.4	615	4	US-08-998-416-186	Sequence 186, App
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	34	42.4	1.4	1186	2	US-08-731-722-5	Sequence 5, Appli
	35	42	1.3	665	2	US-08-883-795A-36	Sequence 36, Appl
	36	42	1.3	1864	4	US-09-468-265-4	Sequence 4, Appli
	37	41.8	1.3	1679	4	US-09-306-060-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,760
; FILING DATE: 19930325
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7409-025-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3232 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 19..2469
US-08-038-760-1

Query Match 99.8%; Score 3105.4; DB 1; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 303

Qy    187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246
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Qy    247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306
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Qy    367 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 426
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Db    844 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 903

Qy    787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846
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Db   1144 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1203

Qy   1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146
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Qy   1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926
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Db   1984 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2043

Qy   1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2044 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2103

Qy   1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2163

Qy   2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2164 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2223

Qy   2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2224 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2283

Qy   2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226
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Db   2284 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2343

Qy   2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286
Db   2344 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2403

Qy   2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346
Db   2404 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2463

Qy   2347 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2406
Db   2464 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2523

Qy   2407 CAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCT 2466
Db   2524 CAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCT 2583

Qy   2467 CTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAA 2526
Db   2584 CTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAA 2643

Qy   2527 ATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAA 2586
Db   2644 ATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAA 2703

Qy   2587 AGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAAAATTGCTGTGCTTTATGGATAGTAAGA 2646
Db   2704 AGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAAAATTGCTGTGCTTTATGGATAGTAAGA 2763

Qy   2647 ATGGCCCTAGAGTGGGAGTCCTGATAACCCAGGCCTGTCTGACTACTTTGCCTTCTTTTG 2706
Db   2764 ATGGCCCTAGAGTGGGAGTCCTGATAACCCAGGCCTGTCTGACTACTTTGCCTTCTTTTG 2823

Qy   2707 TAGCATATAGGTGATGTTTGCTCTTGTTTTTATTAATTTATATGTATATTTTTTTAATTT 2766
Db   2824 TAGCATATAGGTGATGTTTGCTCTTGTTTTTATTAATTTATATGTATATTTTTTTAATTT 2883

Qy   2767 AACATGAACACCCTTAGAAAATGTGTCCTATCTATCTTCCAAATGCAATTTGATTGACTG 2826
Db   2884 AACATGAACACCCTTAGAAAATGTGTCCTATCTATCATCCAAATGCAATTTGATTGACTG 2943

Qy   2827 CCCATTCACCAAAATTATCCTGAACTCTTCTGCAAAAATGGATATTATTAGAAATTAGAA 2886
Db   2944 CCCATTCACCAAAATTATCCTGAACTCTTCTGCAAAAATGGATATTATTAGAAATTAGAA 3003

Qy   2887 AAAAATTACTAATTTTACACATTAGATTTTATTTTACTATTGGAATCTGATATACTGTGT 2946
Db   3004 AAAAATTACTAATTTTACACATTAGATTTTATTTTACTATTGGAATCTGATATACTGTGT 3063

Qy   2947 GCTTGTTTTATAAAATTTTGCTTTTAATTAAATAAAAGCTGGAAGCAAAGTATAACCATA 3006
Db   3064 GCTTGTTTTATAAAATTTTGCTTTTAATTAAATAAAAGCTGGAAGCAAAGTATAACCATA 3123

Qy   3007 TGATACTATCATACTACTGAAACAGATTTCATACCTCAGAATGTAAAAGAACTTACTGAT 3066
Db   3124 TGATACTATCATACTACTGAAACAGATTTCATACCTCAGAATGTAAAAGAACTTACTGAT 3183

Qy   3067 TATTTTCTTCATCCAACTTATGTTTTTAAATGAGGATTATTGATAGT 3113
Db   3184 TATTTTCTTCATCCAACTTATGTTTTTAAATGAGGATTATTGATAGT 3230


RESULT 2
US-08-038-760-2/c
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2

  Query Match             99.8%;  Score 3105.4;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3106;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66
Db    3113 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 3054

Qy      67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126
Db    3053 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 2994

Qy     127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186
Db    2993 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 2934

Qy     187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246
Db    2933 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 2874

Qy     247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306
Db    2873 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 2814

Qy     307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 366
Db    2813 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 2754

Qy     367 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 426
Db    2753 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 2694

Qy     427 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 486
Db    2693 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 2634

Qy     487 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 546
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Db  2633 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 2574

Qy   547 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2573 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 2514

Qy   607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 666
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2513 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 2454

Qy   667 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 726
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2453 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 2394

Qy   727 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 786
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2393 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 2334

Qy   787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2333 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 2274

Qy   847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2273 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 2214

Qy   907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2213 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 2154

Qy   967 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1026
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2153 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 2094

Qy  1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2093 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 2034

Qy  1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2033 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1974

Qy  1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1973 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1914

Qy  1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1913 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1854

Qy  1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1853 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1794

Qy  1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1793 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1734

Qy  1387 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1446
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1733 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1674

Qy  1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1673 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1614

Qy  1507 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1566
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1613 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1554

Qy  1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1553 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1494
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Qy  1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1493 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1434

Qy  1687 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1746
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1433 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1374

Qy  1747 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1806
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1373 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1314

Qy  1807 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1866
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1313 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1254

Qy  1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1253 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1194

Qy  1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1193 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1134

Qy  1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1133 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 1074

Qy  2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1073 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 1014

Qy  2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1013 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 954

Qy  2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   953 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 894

Qy  2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   893 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 834

Qy  2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   833 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 774

Qy  2347 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2406
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   773 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 714

Qy  2407 CAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCT 2466
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   713 CAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCT 654

Qy  2467 CTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAA 2526
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   653 CTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAA 594

Qy  2527 ATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAA 2586
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   593 ATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAA 534

Qy  2587 AGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAAAATTGCTGTGCTTTATGGATAGTAAGA 2646
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   533 AGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAAAATTGCTGTGCTTTATGGATAGTAAGA 474

Qy  2647 ATGGCCCTAGAGTGGGAGTCCTGATAACCCAGGCCTGTCTGACTACTTTGCCTTCTTTTG 2706
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   473 ATGGCCCTAGAGTGGGAGTCCTGATAACCCAGGCCTGTCTGACTACTTTGCCTTCTTTTG 414
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Qy   2707 TAGCATATAGGTGATGTTTGCTCTTGTTTTTATTAATTTATATGTATATTTTTTTAATTT 2766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 TAGCATATAGGTGATGTTTGCTCTTGTTTTTATTAATTTATATGTATATTTTTTTAATTT 354

Qy   2767 AACATGAACACCCTTAGAAAATGTGTCCTATCTATCTTCCAAATGCAATTTGATTGACTG 2826
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    353 AACATGAACACCCTTAGAAAATGTGTCCTATCTATCATCCAAATGCAATTTGATTGACTG 294

Qy   2827 CCCATTCACCAAAATTATCCTGAACTCTTCTGCAAAAATGGATATTATTAGAAATTAGAA 2886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 CCCATTCACCAAAATTATCCTGAACTCTTCTGCAAAAATGGATATTATTAGAAATTAGAA 234

Qy   2887 AAAAATTACTAATTTTACACATTAGATTTTATTTTACTATTGGAATCTGATATACTGTGT 2946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 AAAAATTACTAATTTTACACATTAGATTTTATTTTACTATTGGAATCTGATATACTGTGT 174

Qy   2947 GCTTGTTTTATAAAATTTTGCTTTTAATTAAATAAAAGCTGGAAGCAAAGTATAACCATA 3006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 GCTTGTTTTATAAAATTTTGCTTTTAATTAAATAAAAGCTGGAAGCAAAGTATAACCATA 114

      3007 TGATACTATCATACTACTGAAACAGATTTCATACCTCAGAATGTAAAAGAACTTACTGAT 3066
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       113 TGATACTATCATACTACTGAAACAGATTTCATACCTCAGAATGTAAAAGAACTTACTGAT 54

Qy   3067 TATTTTCTTCATCCAACTTATGTTTTTAAATGAGGATTATTGATAGT 3113
          |||||||||||||||||||||||||||||||||||||||||||||
Db     53 TATTTTCTTCATCCAACTTATGTTTTTAAATGAGGATTATTGATAGT 7


RESULT 3
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1

  Query Match             99.8%;  Score 3105.4;  DB 2;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3106;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 183

Qy     67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 243

Qy    127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 303

Qy    187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 363

Qy    247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 423

Qy    307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 483

Qy    367 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 543

Qy    427 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 603

Qy    487 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    547 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606
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Qy    607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 666
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Db    724 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 783

Qy    667 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 843

Qy    727 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 903

Qy    787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 963

Qy    847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1023

Qy    907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1083
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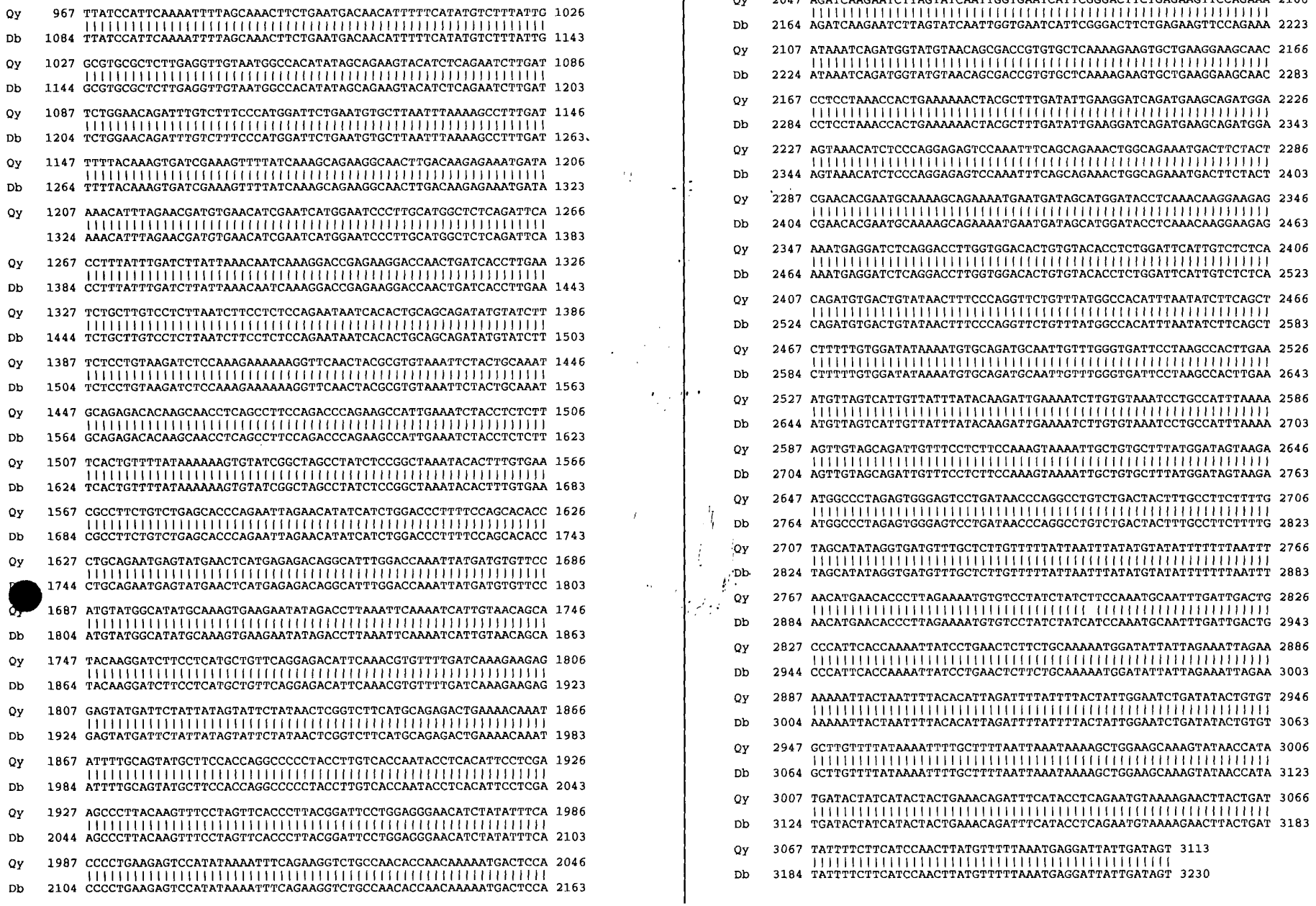
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Db 1084 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1143
Qy 1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086
Db 1144 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1203
Qy 1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146
Db 1204 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1263
Qy 1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206
Db 1264 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1323
Qy 1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
1324 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1383
Qy 1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326
Db 1384 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1443
Qy 1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386
Db 1444 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1503
Qy 1387 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1446
Db 1504 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1563
Qy 1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506
Db 1564 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1623
Qy 1507 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1566
Db 1624 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1683
Qy 1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626
Db 1684 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1743
Qy 1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686
Db 1744 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1803
Qy 1687 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1746
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Qy 1807 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1866
Db 1924 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1983
Qy 1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926
Db 1984 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2043
Qy 1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986
Db 2044 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2103
Qy 1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046
Db 2104 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2163
Qy 2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106
Db 2164 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2223
Qy 2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166
Db 2224 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2283
Qy 2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226
Db 2284 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2343
Qy 2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286
Db 2344 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2403
Qy 2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346
Db 2404 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2463
Qy 2347 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2406
Db 2464 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2523
Qy 2407 CAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCT 2466
Db 2524 CAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCT 2583
Qy 2467 CTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAA 2526
Db 2584 CTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAA 2643
Qy 2527 ATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAA 2586
Db 2644 ATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAA 2703
Qy 2587 AGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAAAATTGCTGTGCTTTATGGATAGTAAGA 2646
Db 2704 AGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAAAATTGCTGTGCTTTATGGATAGTAAGA 2763
Qy 2647 ATGGCCCTAGAGTGGGAGTCCTGATAACCCAGGCCTGTCTGACTACTTTGCCTTCTTTTG 2706
Db 2764 ATGGCCCTAGAGTGGGAGTCCTGATAACCCAGGCCTGTCTGACTACTTTGCCTTCTTTTG 2823
Qy 2707 TAGCATATAGGTGATGTTTGCTCTTGTTTTTATTAATTTATATGTATATTTTTTTAATTT 2766
Db 2824 TAGCATATAGGTGATGTTTGCTCTTGTTTTTATTAATTTATATGTATATTTTTTTAATTT 2883
Qy 2767 AACATGAACACCCTTAGAAAATGTGTCCTATCTATCTTCCAAATGCAATTTGATTGACTG 2826
Db 2884 AACATGAACACCCTTAGAAAATGTGTCCTATCTATCATCCAAATGCAATTTGATTGACTG 2943
Qy 2827 CCCATTCACCAAAATTATCCTGAACTCTTCTGCAAAAATGGATATTATTAGAAATTAGAA 2886
Db 2944 CCCATTCACCAAAATTATCCTGAACTCTTCTGCAAAAATGGATATTATTAGAAATTAGAA 3003
Qy 2887 AAAAATTACTAATTTTACACATTAGATTTTATTTTACTATTGGAATCTGATATACTGTGT 2946
Db 3004 AAAAATTACTAATTTTACACATTAGATTTTATTTTACTATTGGAATCTGATATACTGTGT 3063
Qy 2947 GCTTGTTTTATAAAATTTTGCTTTTAATTAAATAAAAGCTGGAAGCAAAGTATAACCATA 3006
Db 3064 GCTTGTTTTATAAAATTTTGCTTTTAATTAAATAAAAGCTGGAAGCAAAGTATAACCATA 3123
Qy 3007 TGATACTATCATACTACTGAAACAGATTTCATACCTCAGAATGTAAAAGAACTTACTGAT 3066
Db 3124 TGATACTATCATACTACTGAAACAGATTTCATACCTCAGAATGTAAAAGAACTTACTGAT 3183
Qy 3067 TATTTTCTTCATCCAACTTATGTTTTTAAATGAGGATTATTGATAGT 3113
Db 3184 TATTTTCTTCATCCAACTTATGTTTTTAAATGAGGATTATTGATAGT 3230

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RESULT 4
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
       COMPUTER:  IBM PC compatible
       OPERATING SYSTEM:  PC-DOS/MS-DOS
       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2

  Query Match             99.8%;  Score 3105.4;  DB 2;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3106;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66
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Db    3113 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 3054

Qy      67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126
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Db    3053 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 2994

Qy     127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186
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Db    2993 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 2934

Qy     187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246
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Qy     247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306
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Db    2393 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 2334

Qy     787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846
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Db    2333 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 2274

Qy     847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2213 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 2154

Qy     967 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1026
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Db    2153 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 2094

Qy    1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2093 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 2034

Qy    1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2033 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1974

Qy    1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206
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Db    1973 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1914

Qy    1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1913 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1854

Qy    1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326
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Db    1853 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1794

Qy    1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1793 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1734

Qy    1387 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1733 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1674
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Qy   1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1673 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1614

Qy   1507 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1613 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1554

Qy   1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1553 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1494

Qy   1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1493 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1434

Qy   1687 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1433 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1374

Qy   1747 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1373 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1314

Qy   1807 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1254

Qy   1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1194

Qy   1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1134

Qy   1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 1074

Qy   2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 1014

Qy   2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 954

Qy   2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 894

Qy   2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 834

Qy   2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 774

Qy   2347 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 714

Qy   2407 CAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCT 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    713 CAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCT 654

Qy   2467 CTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAA 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    653 CTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAA 594

Qy   2527 ATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAA 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    593 ATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAA 534

Qy   2587 AGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAAAATTGCTGTGCTTTATGGATAGTAAGA 2646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    533 AGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAAAATTGCTGTGCTTTATGGATAGTAAGA 474

Qy   2647 ATGGCCCTAGAGTGGGAGTCCTGATAACCCAGGCCTGTCTGACTACTTTGCCTTCTTTTG 2706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    473 ATGGCCCTAGAGTGGGAGTCCTGATAACCCAGGCCTGTCTGACTACTTTGCCTTCTTTTG 414

Qy   2707 TAGCATATAGGTGATGTTTGCTCTTGTTTTTATTAATTTATATGTATATTTTTTTAATTT 2766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 TAGCATATAGGTGATGTTTGCTCTTGTTTTTATTAATTTATATGTATATTTTTTTAATTT 354

Qy   2767 AACATGAACACCCTTAGAAAATGTGTCCTATCTATCTTCCAAATGCAATTTGATTGACTG 2826
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    353 AACATGAACACCCTTAGAAAATGTGTCCTATCTATCATCCAAATGCAATTTGATTGACTG 294

Qy   2827 CCCATTCACCAAAATTATCCTGAACTCTTCTGCAAAAATGGATATTATTAGAAATTAGAA 2886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 CCCATTCACCAAAATTATCCTGAACTCTTCTGCAAAAATGGATATTATTAGAAATTAGAA 234

Qy   2887 AAAAATTACTAATTTTACACATTAGATTTTATTTTACTATTGGAATCTGATATACTGTGT 2946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 AAAAATTACTAATTTTACACATTAGATTTTATTTTACTATTGGAATCTGATATACTGTGT 174

Qy   2947 GCTTGTTTTATAAAATTTTGCTTTTAATTAAATAAAAGCTGGAAGCAAAGTATAACCATA 3006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 GCTTGTTTTATAAAATTTTGCTTTTAATTAAATAAAAGCTGGAAGCAAAGTATAACCATA 114

Qy   3007 TGATACTATCATACTACTGAAACAGATTTCATACCTCAGAATGTAAAAGAACTTACTGAT 3066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    113 TGATACTATCATACTACTGAAACAGATTTCATACCTCAGAATGTAAAAGAACTTACTGAT 54

Qy   3067 TATTTTCTTCATCCAACTTATGTTTTTAAATGAGGATTATTGATAGT 3113
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Db     53 TATTTTCTTCATCCAACTTATGTTTTTAAATGAGGATTATTGATAGT 7
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RESULT 5
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
```

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;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2

  Query Match             77.6%;  Score 2415;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2415;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

        67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     367 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     427 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

        487 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     547 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     667 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     727 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     967 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    1387 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    1507 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1566
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Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    1687 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    1747 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    1807 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986
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Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy    2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    2347 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2406
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2920 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2979

Qy    2407 CAGATGTGACTGTAT 2421
                 |||||||||||||||
Db    2980 CAGATGTGACTGTAT 2994


RESULT 6
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4

  Query Match             77.6%;  Score 2415;  DB 2;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2415;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 366
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     367 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 426
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     427 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 486
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     487 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 546
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     547 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 666
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     667 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 726
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     727 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 786
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479
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Qy    907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    967 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy   1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy   1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy   1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

     1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy   1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy   1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy   1387 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy   1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy   1507 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy   1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

     1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy   1687 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy   1747 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy   1807 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy   1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy   1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy   1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy   2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy   2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy   2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy   2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy   2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy   2347 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2920 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2979

Qy   2407 CAGATGTGACTGTAT 2421
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Db   2980 CAGATGTGACTGTAT 2994
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RESULT 7
US-08-801-092-3
; Sequence 3, Application US/08801092
; Patent No. 6074850
; GENERAL INFORMATION:
; APPLICANT: Antelman, Douglas
; APPLICANT: Gregory, Richard J.
; APPLICANT: Wils, Kenneth N.
; TITLE OF INVENTION: Tissue Specific Expression of
; TITLE OF INVENTION: Retinoblastoma Protein
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,092
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/751,517
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 016930-001020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 703-576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

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;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-801-092-3

  Query Match             77.6%;  Score 2415;  DB 3;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2415;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

       127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     367 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     427 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     487 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     547 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606
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Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 666
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Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     667 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     727 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     967 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086
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Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
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Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    1387 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    1507 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    1687 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    1747 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    1807 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619
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Qy    2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

      2347 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2920 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2979

Qy    2407 CAGATGTGACTGTAT 2421
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Db    2980 CAGATGTGACTGTAT 2994
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RESULT 8
US-09-315-113-3
; Sequence 3, Application US/09315113
; Patent No. 6379927
;   GENERAL INFORMATION:
;        APPLICANT: Antelman, Douglas
;                   Gregory, Richard J.
;                   Wils, Kenneth N.
;        TITLE OF INVENTION: Tissue Specific Expression of
;                            Retinoblastoma Protein
;        NUMBER OF SEQUENCES: 46
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/315,113
;             FILING DATE: 19-May-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/801,092
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fitts, Renee A.
;             REGISTRATION NUMBER: 35,136
;             REFERENCE/DOCKET NUMBER: 016930-001020
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-576-0200
;             TELEFAX: 703-576-0300
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2994 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;             MOLECULE TYPE: cDNA
;             SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-315-113-3

  Query Match             77.6%;  Score 2415;  DB 4;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2415;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     367 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     427 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     487 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     547 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     667 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     727 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     967 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1026
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Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy   1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy   1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy   1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy   1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy   1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy   1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy   1387 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy   1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy   1507 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy   1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy   1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy   1687 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy   1747 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy   1807 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy   1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy   1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy   1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy   2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy   2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy   2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy   2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy   2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy   2347 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2920 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2979

Qy   2407 CAGATGTGACTGTAT 2421
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Db   2980 CAGATGTGACTGTAT 2994
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RESULT 9
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1
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Query Match             77.5%;  Score 2413.4;  DB 5;  Length 2994;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2414;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

       247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     367 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     427 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     487 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     547 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     667 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     727 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     967 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326
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Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386
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Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    1387 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1446
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Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506
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Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    1507 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1566
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Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626
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Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686
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Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    1687 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1746
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Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    1747 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1806
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Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    1807 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1866
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Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986
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Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046
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Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy    2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106
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Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166
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Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCAGTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286
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Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346
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Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    2347 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2920 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2979

Qy    2407 CAGATGTGACTGTAT 2421
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Db    2980 CAGATGTGACTGTAT 2994


RESULT 10
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
,      TELEPHONE:  (619) 535-9001
,      TELEFAX:  (619) 535-8949
,  INFORMATION FOR SEQ ID NO:  7:
,    SEQUENCE CHARACTERISTICS:
,      LENGTH:  2995 base pairs
,      TYPE:  nucleic acid
,      STRANDEDNESS:  single
,      TOPOLOGY:  linear
,    FEATURE:
,      NAME/KEY:  CDS
,      LOCATION:  139..2922
US-08-959-638-7

  Query Match             77.5%;  Score 2412;  DB 2;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2412;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 366
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Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     547 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606
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Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 666
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Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     667 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 726
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Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

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Qy     847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906
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Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966
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Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     967 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1026
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Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086
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Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146
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Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206
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Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326
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      1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

      1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386
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Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

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Qy    1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506
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Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626
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Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686
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Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

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Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926
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Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046
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Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

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Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226
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Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286
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Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

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Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    2347 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2406
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Db    2920 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2979

Qy    2407 CAGATGTGACTG 2418
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RESULT 11
US-08-328-673A-7
; Sequence 7, Application US/08328673A
; Patent No. 6210939
;   GENERAL INFORMATION:
;       APPLICANT: Gregory, Richard J.
;                  Wills, Ken N.
;                  Maneval, Daniel C.
;       TITLE OF INVENTION: Recombinant Adenoviral Vector and
;                           Methods of Use
;       NUMBER OF SEQUENCES: 9
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/328,673A
;            FILING DATE: 25-Oct-1994
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/142,669
;            FILING DATE: 25-OCT-1993
;            APPLICATION NUMBER: US 08/233,669
;            FILING DATE: 26-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Smith, Timothy S.
;            REGISTRATION NUMBER: 35,367
;            REFERENCE/DOCKET NUMBER: 016930-000920US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2995 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
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;           NAME/KEY:  CDS
;           LOCATION:  139..2925
;           OTHER INFORMATION:  /product= "RB"
;           /note= "retinoblastoma tumor suppressor"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-328-673A-7

  Query Match             77.4%;  Score 2410.4;  DB 4;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2411;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

       127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     367 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     427 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     487 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     547 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     667 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 726
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCTTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     727 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     967 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    1387 TCTCCTGTAAGATCTCCAAAGAAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    1507 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    1687 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    1747 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    1807 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619
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Qy   2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy   2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy   2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy   2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy   2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

     2347 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2920 AAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCA 2979

Qy   2407 CAGATGTGACTG 2418
          ||||||||||||
Db   2980 CAGATGTGACTG 2991
```

RESULT 12
US-07-708-962-1
; Sequence 1, Application US/07708962
; Patent No. 5262321
; GENERAL INFORMATION:
; APPLICANT: Livingston, David M.
; APPLICANT: Ewen, Mark E.
; TITLE OF INVENTION: Tumor Suppressor
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Choate, Hall & Stewart
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/708,962
; FILING DATE: 19910531
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kennedy, Bill
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: DFCI 209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-5020
; TELEFAX: (617) 227-7566
; TELEX: 289374
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2808 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-708-962-1

Query Match 2.2%; Score 68.8; DB 1; Length 2808;
Best Local Similarity 53.1%; Pred. No. 3.6e-07;
Matches 170; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

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Qy   1481 AGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCT 1540
          | | ||||  || | ||   ||  |  |||| ||||| | ||| || ||||   | ||
Db   1940 ACAGGCCAAAGAGAACTGGGTCCTTAGCACTATTTTACAGAAAGGTCTATCATTTGGCAA 1999

Qy   1541 ATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATA 1600
          | | ||  ||  |   || |||   |      |||  ||         || |||  |   |
Db   2000 GTGTACGCTTACGTGATCTATGT---CTAAAACTGGATGTTTCAAATGAGTTACGAAGGA 2056

Qy   1601 TCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGC 1660
            || |||||   |||  |   |||  |      |      ||| || |||| ||||||||
Db   2057 AGATATGGACGTGTTTTGAATTCACTTTAGTTCACTGTCCTGATCTAATGAAAGACAGGC 2116

Qy   1661 ATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACC 1720
          ||||||| ||  |  |  | ||| || | |||  |||     || || |  ||   |||
Db   2117 ATTTGGATCAGCTCCTCCTTTGTGCCTTTTATATCATGGCAAAGGTAACAAAAGAAGAAA 2176

Qy   1721 TTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACAT 1780
            |  ||  ||   ||| | | |   || | | |||  || || |||  |    |   ||
Db   2177 GAACTTTTCAAGAAATTATGAAAAGTTATAGGAATCAGCCCCAAGCTAATAGTCACGTAT 2236

Qy   1781 TCAAACGTGTTTTGATCAAA 1800
          | | ||||| || | |||
Db   2237 ATAGAAGTGTTCTGCTGAAA 2256
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RESULT 13
US-08-106-493A-1
; Sequence 1, Application US/08106493A
; Patent No. 5457049
; GENERAL INFORMATION:
; APPLICANT: Antonio Giordano
; TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN PRB2,
; TITLE OF INVENTION: RELATED GENE PRODUCTS, AND DNA ENCODING
; TITLE OF INVENTION: THEREFOR"
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University-Of The Commonwealth
; ADDRESSEE: System of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,493A
; FILING DATE: August 12, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mullins, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 6056-188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5457049e
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3249 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Single

```
;      TOPOLOGY:  linear
US-08-106-493A-1

  Query Match             2.2%;  Score 68.2;  DB 1;  Length 3249;
  Best Local Similarity   53.0%;  Pred. No. 5.2e-07;
  Matches  170;  Conservative    0;  Mismatches  148;  Indels    3;  Gaps    1;

Qy   1481 AGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCT 1540
          | |  ||   |||  | | |||| | || || || | || ||| || || |   ||||
Db   2312 ATAGACCCAGGAAGACCAGCTCTTTATCGCTTTTCTTTAGAAAGGTATACCATTTAGCAG 2371

Qy   1541 ATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATA 1600
           | |||| ||       || ||||    |   ||   |         |||||     | |
Db   2372 CTGTCCGCCTTCGGGATCTCTGTG---CCAAACTAGATATTTCAGATGAATTGAGGAAAA 2428

Qy   1601 TCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGC 1660
           |||||||||   ||  |   | || |      |      |||||| |||| ||||| |
Db   2429 AAATCTGGACCTGCTTTGAATTCTCCATAATTCAGTGTCCTGAACTTATGATGGACAGAC 2488

     1661 ATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACC 1720
          || |||||||  |  | |||||| |||| |||| ||    || || |  ||   |||
Db   2489 ATCTGGACCAGTTATTAATGTGTGCCATTTATGTGATGGCAAAGGTCACAAAAGAAGATA 2548

Qy   1721 TTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACAT 1780
               ||| | | |||| |       || | |  ||  || || ||        ||   |
Db   2549 AGTCCTTCCAGAACATTATGCGTTGTTATAGGACTCAGCCGCAGGCCCGGAGCCAGGTGT 2608

Qy   1781 TCAAACGTGTTTTGATCAAAG 1801
           | | ||||||||||| ||||
Db   2609 ATAGAAGTGTTTTGATAAAAG 2629


RESULT 14
US-08-429-264-1
; Sequence 1, Application US/08429264
; Patent No. 5532340
;  GENERAL INFORMATION:
;    APPLICANT:  Antonio Giordano
;    TITLE OF INVENTION:  "TUMOR SUPPRESSOR PROTEIN
;    TITLE OF INVENTION:  PRB2"
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seidel, Gonda, Lavorgna & Monaco, P.C.
;      STREET:  1800 Two Penn Center Plaza
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/429,264
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/106,493
;      FILING DATE:  August 12, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, D.A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-188 DI1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5532340e
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3249 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  Single
```

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;      TOPOLOGY:  linear
US-08-429-264-1

  Query Match             2.2%;  Score 68.2;  DB 1;  Length 3249;
  Best Local Similarity   53.0%;  Pred. No. 5.2e-07;
  Matches  170;  Conservative    0;  Mismatches  148;  Indels    3;  Gaps    1;

Qy   1481 AGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCT 1540
          | |  ||   |||  | | |||| | || || || | || ||| || || |   ||||
Db   2312 ATAGACCCAGGAAGACCAGCTCTTTATCGCTTTTCTTTAGAAAGGTATACCATTTAGCAG 2371

Qy   1541 ATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATA 1600
           | |||| ||       || ||||    |   ||   |         |||||     | |
Db   2372 CTGTCCGCCTTCGGGATCTCTGTG---CCAAACTAGATATTTCAGATGAATTGAGGAAAA 2428

Qy   1601 TCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGC 1660
           |||||||||   ||  |   | || |      |      |||||| |||| ||||| |
Db   2429 AAATCTGGACCTGCTTTGAATTCTCCATAATTCAGTGTCCTGAACTTATGATGGACAGAC 2488

Qy   1661 ATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACC 1720
          || |||||||  |  | |||||| |||| |||| ||    || || |  ||   |||
Db   2489 ATCTGGACCAGTTATTAATGTGTGCCATTTATGTGATGGCAAAGGTCACAAAAGAAGATA 2548

Qy   1721 TTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACAT 1780
               ||| | | |||| |       || | |  ||  || || ||        ||   |
Db   2549 AGTCCTTCCAGAACATTATGCGTTGTTATAGGACTCAGCCGCAGGCCCGGAGCCAGGTGT 2608

Qy   1781 TCAAACGTGTTTTGATCAAAG 1801
           | | ||||||||||| ||||
Db   2609 ATAGAAGTGTTTTGATAAAAG 2629


RESULT 15
US-08-832-883-1
; Sequence 1, Application US/08832883
; Patent No. 5807681
;  GENERAL INFORMATION:
;    APPLICANT:  Giordano, Antonio
;    APPLICANT:  Baldi, Alphonso
;    TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS AND PROGNOSIS
;    TITLE OF INVENTION:  OF CANCER
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
;      STREET:  Suite 1800 Two Penn Center Plaza
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,883
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  8321-13 US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4853 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
```

```
;      NAME/KEY:  CDS
;      LOCATION:  70..3489
US-08-832-883-1

  Query Match             2.2%;  Score 68.2;  DB 1;  Length 4853;
  Best Local Similarity   53.0%;  Pred. No. 6e-07;
  Matches  170;  Conservative    0;  Mismatches  148;  Indels    3;  Gaps    1;

Qy    1481 AGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCT 1540
           | |  ||   |||  | | |||| | || || || | || ||| || || |   ||||
Db    2552 ATAGACCCAGGAAGACCAGCTCTTTATCGCTTTTCTTTAGAAAGGTATACCATTTAGCAG 2611

Qy    1541 ATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATA 1600
            | |||| ||       || ||||    |   ||   |         |||||     | |
Db    2612 CTGTCCGCCTTCGGGATCTCTGTG---CCAAACTAGATATTTCAGATGAATTGAGGAAAA 2668

Qy    1601 TCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGC 1660
             |||||||||   ||  |   | || |     |      ||||| |||| ||||| |
Db    2669 AAATCTGGACCTGCTTTGAATTCTCCATAATTCAGTGTCCTGAACTTATGATGGACAGAC 2728

      1661 ATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACC 1720
           || |||||||  |  | |||||| |||| |||| ||    || || |  ||   |||
      2729 ATCTGGACCAGTTATTAATGTGTGCCATTTATGTGATGGCAAAGGTCACAAAAGAAGATA 2788

Qy    1721 TTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACAT 1780
              ||| | | |||| |       || | |  ||  || || ||        ||   |
Db    2789 AGTCCTTCCAGAACATTATGCGTTGTTATAGGACTCAGCCGCAGGCCCGGAGCCAGGTGT 2848

Qy    1781 TCAAACGTGTTTTGATCAAAG 1801
             | | ||||||||||| ||||
Db    2849 ATAGAAGTGTTTTGATAAAAG 2869


Search completed: January 17, 2003, 18:22:00
Job time : 106.88 secs
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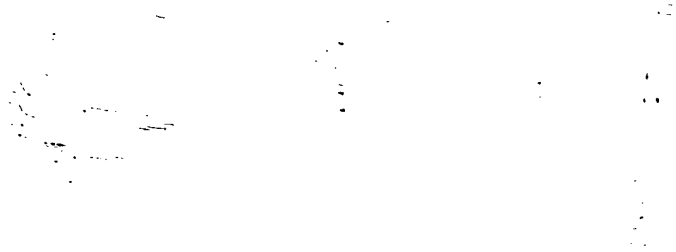

GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 16, 2003, 23:41:58 ; Search time 250.854 Seconds
(without alignments)
7011.280 Million cell updates/sec

Title: US-09-026-459A-37
Perfect score: 4017
Sequence: 1 MSRLLKKYDVLFALFSKLER.....TRMQKQKMNDSMDTSNKEEK 781

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

ched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09026459/runat_16012003_152137_23299/app_query.fasta_1.13467
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09026459_@CGN_1_1_2527_@runat_16012003_152137_23299 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4017	100.0	2994	11	AAQ04713	Cancer supressing
2	4017	100.0	2994	14	AAQ41545	Retinoblastoma gen
3	4017	100.0	2994	19	AAV40004	Retinoblastoma pro
4	4017	100.0	2994	21	AAZ40287	Wild type human re
5	4017	100.0	2995	20	AAX90350	Human p110-RB reti
6	4017	100.0	2995	20	AAX00737	cDNA encoding a re
7	4017	100.0	2995	22	AAH25755	Retinoblastoma tum
8	4017	100.0	2995	22	AAD04474	Retinoblastoma tum
9	4017	100.0	2995	23	ABL50904	Retinoblastoma tum
10	4017	100.0	3113	19	AAV58445	Modified retinobla
11	4017	100.0	3218	19	AAV54991	DNA sequence of th
12	4017	100.0	3233	15	AAQ72690	Retinoblastoma 94k
13	4017	100.0	3266	19	AAV58444	Modified retinobla
14	4017	100.0	3323	19	AAV58443	Modified retinobla
15	4017	100.0	3323	19	AAV58446	Modified retinobla
16	4017	100.0	3392	19	AAV58442	Modified retinobla
17	4017	100.0	3455	19	AAV58441	Modified retinobla
18	4017	100.0	3461	19	AAV58447	Modified retinobla
19	4017	100.0	3554	19	AAV58452	Modified retinobla
20	4017	100.0	3555	19	AAV58440	Modified retinobla
21	4017	100.0	3555	19	AAV54990	DNA sequence of th
22	4017	100.0	4839	21	AAA29391	Human retinoblasto
23	4017	100.0	4839	21	AAZ88444	Human androgen rec
24	4017	100.0	4839	24	ABL62873	Breast cancer rela
25	4014	99.9	4597	9	AAN81369	Human retinoblasto
26	4013	99.9	2995	16	AAQ90059	Retinoblastoma tum
27	4013	99.9	4597	15	AAQ70536	Human retinoblasto
28	4011	99.9	4740	24	ABK86079	Human retinoblasto
29	4010	99.8	4597	20	AAX04501	Human retinoblasto
30	4002	99.6	2995	16	AAQ86398	Human Rb110 cDNA.
31	3903	97.2	5056	10	AAN90489	cDNA of human reti
32	3875	96.5	4579	9	AAN81261	Probe for retinobl
33	3850	95.8	3347	19	AAV58448	Modified retinobla
34	3674.5	91.5	3377	19	AAV58450	Modified retinobla
35	3667.5	91.3	3383	19	AAV58451	Modified retinobla
36	3550	88.4	3161	19	AAV58449	Modified retinobla
37	1761.5	43.9	18303	20	AAX04502	Human retinoblasto
38	1685.5	42.0	18177	10	AAN90490	DNA of human retin
39	772	19.2	3960	24	ABK83840	Human cDNA differe
40	771	19.2	4130	24	AAS94981	Human DNA sequence
41	756	18.8	2808	13	AAQ32665	Nearly complete p1
42	729.5	18.2	4853	24	ABK84660	Human cDNA differe
43	728.5	18.1	3249	16	AAQ8274B	pRb2 retinoblastom
44	605.5	15.1	3291	23	AAS83193	DNA encoding novel
45	519.5	12.9	3210	23	ABL12861	Drosophila melanog

ALIGNMENTS

RESULT 1
AAQ04713
ID AAQ04713 standard; cDNA; 2994 BP.
XX
AC AAQ04713;
XX
DT 11-OCT-1990 (first entry)
XX
DE Cancer supressing gene (CSG).
XX
KW Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW RB; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 139..2922
FT /*tag= a

```
XX
PN   WO9005180-A.
XX
PD   17-MAY-1990.
XX
PF   30-OCT-1989;   89WO-0004808.
XX
PR   31-OCT-1988;   88US-0265829.
XX
PA   (REGC ) UNIV OF CAIFORNIA.
XX
PI   Lee WH,  Huang HJS;
XX
DR   WPI; 1990-178822/23.
DR   P-PSDB; AAR05305.
XX
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
XX
[redacted] Claim 35; Page 86; 105pp; English.
XX
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
XX
SQ   Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          2994
Score:                    4017.00        Matches:         781
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       11             Gaps:            0

US-09-026-459A-37 (1-781) x AAQ04713 (1-2994)

Qy      1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy     21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy    101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy    121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    361 SerGlyThrAspLeuSerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199
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Qy     541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy     561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy     581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy     681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy     701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy     721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy     741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy     781 Lys 781
           |||
Db    2920 AAA 2922
```

RESULT 2
AAQ41545
ID AAQ41545 standard; DNA; 2994 BP.
XX
AC AAQ41545;
XX
DT 24-AUG-1993 (first entry)
XX
DE Retinoblastoma gene.
XX
KW RB gene product; p56RB portion; cell cycle progression control;
KW combination; therapeutic methods; arrest; tumourigenesis;
KW regulation; physiological processes; blood cell prodn.;
KW gamete prodn.; ss.
XX
OS Homo sapiens SR-40 cell line.
XX
FH Key   Location/Qualifiers
FT CDS   139..2925
FT   /*tag= a
FT   /note= "Rb protein"
XX
PN WO9308267-A.
XX
PD 29-APR-1993.
XX
PF 16-OCT-1992; 92WO-US08918.
XX
PR 17-OCT-1991; 91US-0778510.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Goodrich DW, Lee EYHP, Lee WH, Wang NP;
XX
DR WPI; 1993-152462/18.
DR P-PSDB; AAR36534.
XX
PT Method of controlling cell cycle progression - uses purified
PT retinoblastoma protein or fragment, for use in combination with
PT therapeutic methods to arrest tumorigenesis
XX
PS Disclosure; Fig 9; 68pp; English.
XX
CC The sequence is that of the retinoblastoma gene which encodes the
CC retinoblastoma (RB) protein which may be used as part of a method of
CC controlling cell cycle progression which may be used in combination
CC with therapeutic methods to arrest tumourigenesis in organisms. The
CC cell cycle can be reversibly arrested in a convenient and safe
CC manner. The protein is used in a compsn. is relatively inexpensive
CC and readily obtainable, and shows little or no toxic effects on
CC healthy cells. It is also compatible with other methods and devices
CC for regulating certain physiological processes of the body, such as
CC blood cell prodn. and gamete prodn. Fragments of the protein are
CC soluble in low concns. of glycerol thus enhancing their value in
CC pharmaceutical applicns.
XX
SQ Sequence 2994 BP; 974 A; 618 C; 594 G; 808 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	2994
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-026-459A-37 (1-781) x AAQ41545 (1-2994)

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Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160

Db   1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180

Db   1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200

Db   1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220

Db   1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240

I    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260

Db   1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280

Db   1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300

Db   1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320

Db   1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340

Db   1540 TTATCCATTCAAAATTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360

Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380

I    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400

Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420

Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440

Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460

Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480

Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500

Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520

Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540

Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560

Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580

Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600

Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620

Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640

Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660

Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680

Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700

Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720

Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740

Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760

Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780

Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    781 Lys 781

Db   2920 AAA 2922

RESULT 3
AAV40004
ID   AAV40004 standard; DNA; 2994 BP.
XX
AC   AAV40004;
XX
DT   15-FEB-1999  (first entry)
XX
DE   Retinoblastoma protein RB.
XX
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
```

KW thyroid hyperplasia; Grave's disease; psoriasis;
KW benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW peripheral vascular disease; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 139..2925
FT /*tag= a
XX
PN WO9821228-A1.
XX
PD 22-MAY-1998.
XX
PF 13-NOV-1997; 97WO-US21821.
XX
PR 14-FEB-1997; 97US-0801092.
PR 15-NOV-1996; 96US-0751517.
XX
PA (CANJ-) CANJI INC.

Antelman D, Gregory RJ, Wills KN;

DR WPI; 1998-297858/26.
DR P-PSDB; AAW62465.
XX
PT New fusion polypeptide of, e.g. transcription factor - used to
PT treat, e.g. hyper-proliferative disease such as cancer and
PT restenosis
XX
PS Example 1; Fig 2A; 91pp; English.
XX
CC This nucleotide sequence includes a coding region for retinoblastoma
CC protein RB (see AAW62465). A new claimed polypeptide is a fusion of:
CC (1) a transcription factor (TF) comprising a DNA binding domain,
CC and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC suppression domain. Also new are: (1) a nucleic acid encoding the
CC fusion protein, and (2) expression vectors containing such DNA.
CC The fusion protein, particularly expressed from gene therapy
CC vectors (especially adenovirus vectors), is used to treat
CC hyperproliferative conditions, specifically cancer (particularly of
CC the bladder) or restenosis (after angioplasty), but also diabetic
CC retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC vascular disease. Tissue-specific expression of E2F-RB fusions is
CC provided. The fusion proteins are more effective in repressing
CC transcription of the E2F promoter than Rb alone and cause cell-cycle
CC arrest in a variety of cells.
XX
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	2994
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-09-026-459A-37 (1-781) x AAV40004 (1-2994)

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Qy      1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy     21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy    101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy    121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
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Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460

Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480

Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500

Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520

Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540

Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560

Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580

Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600

Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620

Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640

Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660

Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680

Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700

Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720

Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740

Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760

Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780

Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    781 Lys 781
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Db   2920 AAA 2922

RESULT 4
AAZ40287
ID   AAZ40287 standard; cDNA; 2994 BP.
XX
AC   AAZ40287;
XX
DT   24-FEB-2000  (first entry)
XX
DE   Wild type human retinoblastoma gene.
XX
KW   RB gene; human; retinoblastoma gene; mutation detection; immunoscreening;
KW   retinoblastoma diagnosis; hereditary retinoblastoma; secondary cancer;
KW   osteosarcoma; fibrosarcoma; glioblastoma; breast cancer;
KW   tumourigenesis suppression; ss.
XX
OS   Homo sapiens.
XX
PN   US5998134-A.
XX
PD   07-DEC-1999.
XX
PF   07-JUN-1995;   95US-0482627.
XX
PR   15-OCT-1987;   87US-0108748.
PR   28-SEP-1992;   92US-0951947.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lee EYP,  Lee W;
XX
DR   WPI; 2000-052540/04.
DR   P-PSDB; AAY55060.
XX
PT   Detecting retinoblastoma gene-cancer in mammals -
XX
PS   Example 6; Fig 7; 34pp; English.
XX
CC   This sequence represents the wild type human retinoblastoma gene.
CC   The invention relates to a method of detecting a mutated retinoblastoma
CC   (mRB) nucleic acid in mammals comprising hybridizing an isolated
CC   full-length, wild-type RB (wtRB) cDNA probe to a cell sample and
CC   detecting a mutated RB nucleic acid. The method is useful as a diagnostic
CC   tool for diagnosing retinoblastoma. RB cDNA or genomic DNA are preferably
CC   used as probes to determine the defect region of the mRB gene through
CC   genomic DNA blotting analysis or using the method of restriction fragment
CC   length polymorphism analysis to determine the diseased allele. Cloned RB
CC   cDNA can be used to generate specific anti-RB protein (anti-ppRB110)
CC   antibodies which are useful for immunoscreening of tissue biopsy. The
CC   diagnostic method is particularly intended for use in screening
CC   families with a history of hereditary retinoblastoma and for screening
CC   their children. It may also be used in prophylactic and postnatal
CC   screening and for the prediction of the development of secondary
CC   cancer, such as, osteosarcoma, fibrosarcoma, glioblastoma, breast
CC   cancer whether or not connected with retinoblastoma. The method is also
CC   used in the suppression of tumourigenesis where the absent RB protein
CC   ppRB110 will be provided through the molecular induction and gene
CC   transplanting of the RB cDNA to the individual in need of ppRB110.
XX
SQ   Sequence 2994 BP; 974 A; 618 C; 594 G; 808 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          2994
Score:                    4017.00        Matches:         781
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       21             Gaps:            0

US-09-026-459A-37 (1-781) x AAZ40287 (1-2994)

Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
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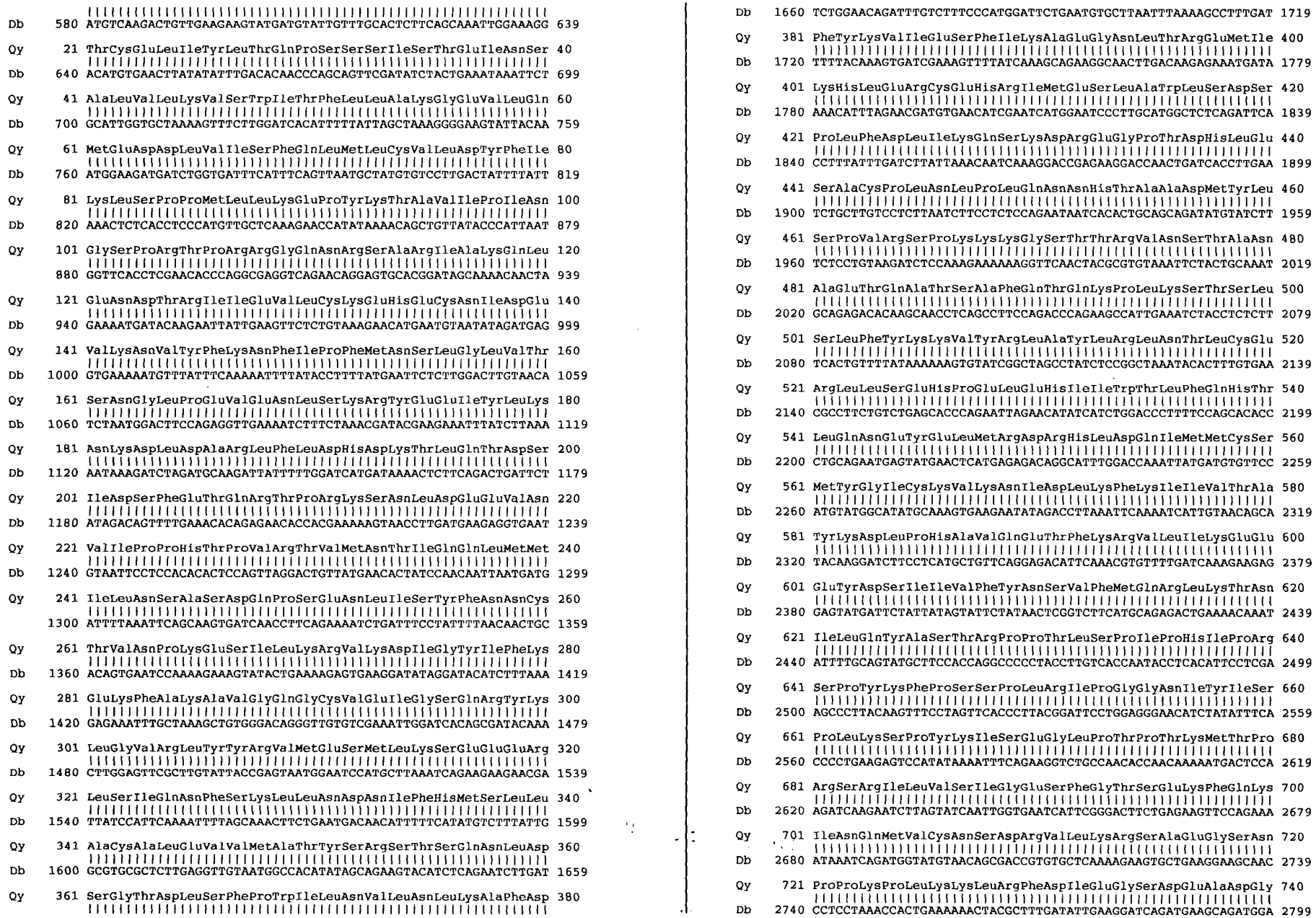
Db 580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639
Qy 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
Db 640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699
Qy 41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
Db 700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759
Qy 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
Db 760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819
Qy 81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
Db 820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879
Qy 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939
Qy 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
Db 940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999
Qy 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
Db 1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059
Qy 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
Db 1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119
Qy 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db 1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179
Qy 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
Db 1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239
Qy 221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
Db 1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299
Qy 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359
Qy 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
Db 1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419
Qy 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
Db 1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479
Qy 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
Db 1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539
Qy 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
Db 1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599
Qy 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
Db 1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659
Qy 361 SerGlyThrAspLeuSerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
Db 1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719
Qy 381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
Db 1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779
Qy 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
Db 1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839
Qy 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
Db 1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899
Qy 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
Db 1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959
Qy 461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
Db 1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019
Qy 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db 2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079
Qy 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
Db 2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139
Qy 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
Db 2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTCCAGCACACC 2199
Qy 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
Db 2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259
Qy 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
Db 2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319
Qy 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
Db 2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379
Qy 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
Db 2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439
Qy 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
Db 2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499
Qy 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
Db 2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559
Qy 661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
Db 2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619
Qy 681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
Db 2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679
Qy 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
Db 2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739
Qy 721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
Db 2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

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Qy     741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
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Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy     781 Lys 781
           |||
Db    2920 AAA 2922

RESULT 5
AAX90350
ID   AAX90350 standard; cDNA; 2995 BP.
XX
AC   AAX90350;
XX
[redacted]  27-SEP-1999  (first entry)

DE   Human p110-RB retinoblastoma tumour suppressor encoding cDNA.
XX
KW   Human; p110-RB; retinoblastoma; tumour suppressor; gene therapy;
KW   adenoviral protein IX; recombinant adenovirus expression vector;
KW   cell cycle; p53; mitosin; cell death; apoptosis; thymidine kinase;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             139..2925
FT                   /*tag= a
FT                   /product= "p110-RB"
FT                   /note= "retinoblastoma tumour suppressor"
XX
PN   US5932210-A.
XX
PD   03-AUG-1999.
XX
PF   28-OCT-1997;   97US-0959638.
XX
PR   25-OCT-1994;   94US-0328673.
PR   25-OCT-1993;   93US-0142669.
PR   19-MAY-1994;   94US-0246006.
PR   28-OCT-1997;   97US-0959638.
XX
[redacted]  (CANJ-) CANJI INC.
[redacted]
PI   Gregory RJ,  Maneval DC,  Wills KN;
XX
DR   WPI; 1999-443568/37.
DR   P-PSDB; AAY24471.
XX
PT   Recombinant adenoviral vectors useful for gene therapy of cancer,
PT   especially p53 deficient tumours
XX
PS   Disclosure; Fig 3; 50pp; English.
XX
CC   The present invention describes a composition comprising a recombinant
CC   adenovirus expression vector, where the vector has an insert of
CC   exogenous DNA comprising a gene encoding a foreign protein and
CC   adenovirus DNA in which all of the coding sequences of E1a, E1b, and
CC   protein IX, and part of E3 are deleted. The vectors are useful in gene
CC   therapy treatment of cancer, especially for treating p53 deficient
CC   tumours. The vector enables safer and more efficient gene therapy of
CC   cancer. The present sequence encodes human p110-RB retinoblastoma
CC   tumour suppressor which can be used as the foreign gene in the above
CC   vector.
XX
SQ   Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:

Pred. No.:                0          Length:          2995
Score:                    4017.00    Matches:         781
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0
Query Match:              100.00%    Indels:          0
DB:                       20         Gaps:            0

US-09-026-459A-37 (1-781) x AAX90350 (1-2995)

Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
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Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539
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Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
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Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    361 SerGlyThrAspLeuSerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

     421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    781 Lys 781
          |||
Db   2920 AAA 2922

RESULT 6
AAX00737
ID   AAX00737 standard; cDNA; 2995 BP.
XX
AC   AAX00737;
XX
DT   13-APR-1999  (first entry)
XX
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
XX
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             139..2925
FT                   /*tag= a
FT                   /product= RB_protein
FT                   /transl_except= (pos: 226..228, aa: Glu)
XX
PN   US5851991-A.
XX
PD   22-DEC-1998.
XX
PF   13-SEP-1994;   94US-0306513.
XX
PR   13-SEP-1994;   94US-0306513.
PR   31-AUG-1987;   87US-0091547.
PR   17-SEP-1987;   87US-0098612.
PR   15-OCT-1987;   87US-0108748.
PR   31-OCT-1988;   88US-0265829.
PR   11-JUL-1990;   90US-0550877.
PR   16-JUL-1990;   90US-0553892.
PR   16-JUL-1990;   90US-0553905.
PR   17-OCT-1991;   91US-0778510.
PR   14-JUL-1992;   92US-0914039.
PR   02-OCT-1992;   92US-0956472.
PR   17-JUN-1993;   93US-0079207.
PR   13-SEP-1993;   93US-0121108.
PR   24-SEP-1993;   93US-0126810.
XX
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Goodrich DW,  Johnson D,  Lee EY,  Lee W,  Shepard HM;
PI   Wang NP;
XX
DR   WPI; 1999-080477/07.
```

```
DR   P-PSDB; AAW67801.
XX
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
XX
PS   Example 1; Fig 2A-K; 72pp; English.
XX
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
XX
SQ   Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:
[redacted]. No.:              0              Length:          2995
[redacted]e:                  4017.00        Matches:         781
Percent Similarity:           100.00%        Conservative:    0
Best Local Similarity:        100.00%        Mismatches:      0
Query Match:                  100.00%        Indels:          0
DB:                           20             Gaps:            0

US-09-026-459A-37 (1-781) x AAX00737 (1-2995)

Qy      1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy     21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGAAGTATTACAA 759

Qy     61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

      101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy    121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy     681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

       701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy     721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy     741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy     781 Lys 781
          |||
Db    2920 AAA 2922

RESULT 7
AAH25755
ID   AAH25755 standard; DNA; 2995 BP.
XX
AC   AAH25755;
XX
     14-AUG-2001  (first entry)

     Retinoblastoma tumour suppressor gene.
XX
KW   Retinoblastoma; tumour suppressor protein; Rb; p53; cancer;
KW   adenoviral vector; gene therapy; thymidine kinase; ds.
XX
OS   Unidentified.
XX
PN   US2001006629-A1.
XX
PD   05-JUL-2001.
XX
PF   24-NOV-1999;   99US-0449113.
XX
PR   25-OCT-1994;   94US-0328673.
PR   25-OCT-1993;   93US-0142669.
PR   19-MAY-1994;   94US-0246006.
XX
PA   (GREG/) GREGORY R J.
PA   (WILL/) WILLS K N.
PA   (MANE/) MANEVAL D C.
XX
PI   Gregory RJ,  Wills KN,  Maneval DC;
XX
DR   WPI; 2001-397210/42.
DR   P-PSDB; AAB98945.
XX
PT   Recombinant adenovirus expression vector comprising a partial or total
PT   deletion of a protein IX DNA and a gene encoding a foreign protein e.g.
PT   suicide protein, useful for inhibiting or reducing the proliferation of
PT   a tumour e.g. brain tumour -
XX
PS   Disclosure; Fig 3; 39pp; English.
XX
CC   The present invention describes an adenoviral expression vector
CC   comprising a deletion in the protein IX gene and a gene encoding a
CC   foreign protein. This vector can be used in gene therapy, particularly to
CC   introduce tumour suppressor genes into cancerous cells. Genes which may
CC   be used include p53, thymidine kinase and retinoblastoma tumour
CC   suppressor gene (Rb). The present sequence is the retinoblastoma tumour
CC   suppressor gene.
XX
SQ   Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:
Pred. No.:              0           Length:         2995
Score:                  4017.00     Matches:        781
Percent Similarity:     100.00%     Conservative:   0
Best Local Similarity:  100.00%     Mismatches:     0
Query Match:            100.00%     Indels:         0
DB:                     22          Gaps:           0

US-09-026-459A-37 (1-781) x AAH25755 (1-2995)

Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239
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Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TTATCCATTCAAAATTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
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Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    781 Lys 781
          |||
Db   2920 AAA 2922
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RESULT 8
AAD04474
ID AAD04474 standard; cDNA; 2995 BP.
XX
AC AAD04474;
XX
DT 04-JUL-2001 (first entry)
XX
DE Retinoblastoma tumour suppressor protein, p110RB cDNA.
XX
KW Retinoblastoma; RB; tumour suppressor protein; p110RB; p53; gene therapy;
KW cytostatic; antithyroid; antipsoriatic; adenoviral protein IX; psoriasis;
KW thyroid hyperplasia; Grave's disease; hepatocellular carcinoma; neoplasm;
KW benign prostatic hypertrophy; Li-Fraumeni syndrome; sickle cell anaemia;
KW Tay-Sachs disease; leukaemia; lymphoma; adenovirus vector; cancer; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 139..2925
FT /*tag= a
FT /product= "Retinoblastoma tumour suppressor protein,
FT p110RB"
XX
PN US6210939-B1.
XX
PD 03-APR-2001.
XX
PF 25-OCT-1994; 94US-0328673.

```
XX
PR   25-OCT-1993;   93US-0142669.
PR   19-MAY-1994;   94US-0233777.
XX
PA   (CANJ-) CANJI INC.
XX
PI   Gregory RJ,  Wills KN,  Maneval DC;
XX
DR   WPI; 2001-289633/30.
DR   P-PSDB; AAE00689.
XX
PT   New recombinant adenovirus expression vector having a gene encoding for
PT   a foreign protein and a partial or total deletion of the adenoviral
PT   protein IX DNA, useful in gene therapy for treating or reducing
PT   hyperproliferative cells -
XX
PS   Disclosure; Fig 3; 49pp; English.
XX
CC   The present cDNA sequence encodes retinoblastoma (RB) tumour suppressor
CC   protein, designated as p110RB.
CC   The invention relates to a recombinant adenovirus expression vector
CC   characterised by the partial or total deletion of the adenoviral protein
CC   IX DNA beginning at nucleotides 357 or 360 and ending at 4020-4050, and
CC   having a gene encoding a foreign protein such as tumour suppressor
CC   protein, p110RB (retinoblastoma) and p53. Adenovirus vector is used
CC   for screening tumour suppressor genes useful in gene therapy. The vector
CC   is particularly useful for treating or reducing hyperproliferative cell
CC   disorders such as thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome, cancers specifically
CC   hepatocellular carcinoma, neoplasms, leukaemias, lymphomas, etc. to
CC   inhibit tumour proliferation or to ameliorate particular related
CC   pathology such as sickle cell anaemia and Tay-Sachs disease. The vector
CC   is also useful for the safe recombinant production of diagnostic and
CC   therapeutic polypeptides and proteins.
XX
SQ   Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          2995
Score:                    4017.00        Matches:         781
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       22             Gaps:            0

US-09-026-459A-37 (1-781) x AAD04474 (1-2995)

Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
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Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
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Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy     341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy     361 SerGlyThrAspLeuSerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy     381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy     401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy     421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy     441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
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Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy     461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy     481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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Qy     501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy     521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy     541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy     561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy     581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
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Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy     681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy     701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
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Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy     721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy     741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy     781 Lys 781
           |||
Db    2920 AAA 2922
```

RESULT 9
ABL50904
ID ABL50904 standard; cDNA; 2995 BP.
XX
AC ABL50904;
XX
DT 24-JUN-2002 (first entry)
XX
DE Retinoblastoma tumour suppressor protein p110-RB encoding cDNA.
XX
KW Retinoblastoma; tumour suppressor protein; p110-RB; cell cycle; p53;
KW Rb; mitosin; cell death; adenoviral protein IX; gene therapy; cytostatic;
KW adenovirus expression vector; tumour; non-small cell lung cancer;
KW small cell lung cancer; hepatocarcinoma; hepatocellular carcinoma;
KW melanoma; retinoblastoma; colorectal carcinoma; sarcoma; Wilm's tumour;
KW astrocytoma; glioblastoma; neuroblastoma; ovarian carcinoma;
KW osteosarcoma; renal cancer; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   139..2925
FT   /*tag= a
FT   /product= "retinoblastoma tumour suppressor protein"
XX
PN US2001016192-A1.
XX
PD 23-AUG-2001.
XX
PF 28-OCT-1997; 97US-0958570.
XX
PR 25-OCT-1994; 94US-0328673.
PR 25-OCT-1993; 93US-0142669.
PR 26-APR-1994; 94US-0233777.
XX
PA (GREG/) GREGORY R J.
PA (WILL/) WILLS K N.
PA (MANE/) MANEVAL D C.
XX
PI Gregory RJ, Wills KN, Maneval DC;
XX
DR WPI; 2001-535532/59.
DR P-PSDB; ABB07055.
XX
PT New recombinant adenoviral vector comprising a partial or total
PT deletion of a protein IX DNA and a gene encoding a foreign protein,
PT useful in gene therapy, particularly for treating or suppressing
PT proliferation of a tumor -
XX
PS Disclosure; Fig 3; 37pp; English.
XX
CC The present invention describes a recombinant adenovirus expression
CC vector, which comprises a partial or total deletion of a protein IX DNA
CC and a gene encoding a foreign protein. The recombinant adenovirus vector
CC can have cytostatic activity and be used in gene therapy. The recombinant
CC adenovirus expression vector is particularly useful for treating or
CC suppressing proliferation of a tumour, e.g. non-small cell lung cancer,
CC small cell lung cancer, hepatocarcinoma or hepatocellular carcinoma,
CC melanoma, retinoblastoma, breast tumour, colorectal carcinoma, sarcoma,
CC prostate tumour, bladder tumour, tumour of the reticuloendothelial
CC tissues, Wilm's tumour, astrocytoma, glioblastoma, neuroblastoma,
CC ovarian carcinoma, osteosarcoma or renal cancer. The present sequence
CC encodes the retinoblastoma tumour suppressor protein p110-RB, which is
CC given in the exemplification of the present invention.
XX
SQ Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	2995
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	23	Gaps:	0

US-09-026-459A-37 (1-781) x ABL50904 (1-2995)

```
Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699
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Qy     41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
Db    700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
Db    760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
Db    820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy    101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
Db    880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy    121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
Db    940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
Db   1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
Db   1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db   1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
Db   1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
Db   1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
Db   1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
Db   1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
Db   1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
Db   1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
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Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
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Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    781 Lys 781
          |||
Db   2920 AAA 2922

RESULT 10
AAV58445
ID   AAV58445 standard; DNA; 3113 BP.
XX
AC   AAV58445;
XX
DT   02-DEC-1998  (first entry)
XX
DE   Modified retinoblastoma tumour suppressor gene.
XX
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7..2352
FT                   /*tag=  a
XX
PN   WO9837091-A2.
XX
PD   27-AUG-1998.
XX
PF   19-FEB-1998;   98WO-US03041.
XX
PR   20-FEB-1997;   97US-0038118.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Benedict WF,  Hu S,  Xu H,  Zhou Y;
XX
DR   WPI; 1998-480788/41.
DR   P-PSDB; AAW69369.
XX
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
XX
PS   Claim 22; Page 173-177; 249pp; English.
XX
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
XX
SQ   Sequence 3113 BP; 1039 A; 577 C; 547 G; 950 T; 0 other;

Alignment Scores:
Pred. No.:              0              Length:         3113
Score:                  4017.00        Matches:        781
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     19             Gaps:           0

US-09-026-459A-37 (1-781) x AAV58445 (1-3113)

Qy      1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66

Qy     21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126

Qy     41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186

Qy     61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246

Qy     81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306

Qy    101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 366

Qy    121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 426

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 486

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 546

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 666

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 726

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 786

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1026

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086

Qy    361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
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Db   1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440

Db   1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460

Db   1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480

Db   1387 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1446

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500

Db   1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520

Db   1507 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1566

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540

Db   1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560

Db   1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580

Db   1687 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1746

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600

Db   1747 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1806

Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620

Db   1807 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1866

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640

Db   1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926

Qy    641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660

Db   1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680

Db   1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700

Db   2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720

Db   2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740

Db   2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760

Db   2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780

Db   2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346

Qy    781 Lys 781
           |||
Db   2347 AAA 2349
```

RESULT 11
AAV54991
ID AAV54991 standard; DNA; 3218 BP.
XX
AC AAV54991;
XX
DT 26-NOV-1998 (first entry)
XX
DE DNA sequence of the specification.
XX
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 7..2457
FT /*tag= a
XX
PN WO9837185-A2.
XX
PD 27-AUG-1998.
XX
PF 19-FEB-1998; 98WO-US03092.
XX
PR 20-FEB-1997; 97US-0038755.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
XX
DR WPI; 1998-480796/41.
DR P-PSDB; AAW71355.
XX
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
XX
PS Disclosure; Pages 153-157; 190pp; English.
XX
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
XX
SQ Sequence 3218 BP; 1080 A; 595 C; 561 G; 982 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	3218
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-09-026-459A-37 (1-781) x AAV54991 (1-3218)

```
Qy      1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg  20
Db    112 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 171

Qy     21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer  40
Db    172 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 231

Qy     41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln  60
Db    232 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 291

Qy     61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle  80
Db    292 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 351

Qy     81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
Db    352 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 411

Qy    101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
Db    412 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 471

Qy    121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
Db    472 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 531

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
Db    532 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 591

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
Db    592 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 651

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db    652 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 711

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
Db    712 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 771

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
Db    772 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 831

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
Db    832 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 891

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
Db    892 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 951

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
Db    952 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1011

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
Db   1012 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1071

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
Db   1072 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1131

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
Db   1132 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1191

Qy    361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
Db   1192 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1251

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
Db   1252 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1311

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
Db   1312 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1371

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
Db   1372 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1431

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
Db   1432 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1491

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
Db   1492 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1551

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db   1552 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1611

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
Db   1612 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1671

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
Db   1672 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1731

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
Db   1732 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1791

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
Db   1792 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1851

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
Db   1852 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1911

Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
Db   1912 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1971

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
Db   1972 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2031

Qy    641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
Db   2032 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2091

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
Db   2092 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2151

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
Db   2152 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2211

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
Db   2212 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2271

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
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Db   2272 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2331

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760

Db   2332 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2391

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780

Db   2392 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2451

Qy    781 Lys 781
Db   2452 AAA 2454

RESULT 12
AAQ72690
ID   AAQ72690 standard; DNA; 3233 BP.
XX
AC   AAQ72690;

     01-JUN-1995  (first entry)

DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
XX
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             19..2469
FT                   /*tag=  a
XX
PN   WO9421115-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03211.
XX
PR   25-MAR-1993;   93US-0038760.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Benedict WF,  Xu H,  Xu S;
XX
DR   WPI; 1994-316534/39.
DR   P-PSDB; AAR63564.
XX
     Broad spectrum tumour suppressor gene - by using retinoblastoma
     gene product p94RB to suppress abnormal cell proliferation in the
     treatment of cancer
XX
PS   Claim 4; Fig 1; 115pp; English.
XX
CC   AAQ72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   AAR63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. AAR63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
XX
SQ   Sequence 3233 BP; 1086 A; 597 C; 567 G; 983 T; 0 other;

Alignment Scores:
Pred. No.:              0              Length:          3233
Score:                  4017.00        Matches:         781
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     15             Gaps:            0

US-09-026-459A-37 (1-781) x AAQ72690 (1-3233)

Qy      1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20

Db    124 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 183

Qy     21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40

Db    184 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 243

Qy     41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60

Db    244 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 303

Qy     61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80

Db    304 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 363

Qy     81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100

Db    364 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 423

Qy    101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120

Db    424 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 483

Qy    121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140

Db    484 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 543

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160

Db    544 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 603

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180

Db    604 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 663

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200

Db    664 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 723

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220

Db    724 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 783

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240

Db    784 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 843

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260

Db    844 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 903

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280

Db    904 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 963

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300

Db    964 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1023

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320

Db   1024 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1083

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340

Db   1084 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1143

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360

Db   1144 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1203
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Qy     361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1204 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1263

Qy     381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1264 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1323

Qy     401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1324 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1383

Qy     421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1384 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1443

Qy     441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1444 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1503

           461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1504 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1563

Qy     481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1564 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1623

Qy     501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1624 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1683

Qy     521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1684 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1743

Qy     541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1744 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1803

Qy     561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1804 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1863

Qy     581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1864 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1923

           601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1924 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1983

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1984 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2043

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2044 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2103

Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2104 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2163

Qy     681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2164 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2223

Qy     701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2224 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2283

Qy     721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2284 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2343

Qy     741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2344 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2403

Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2404 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2463

Qy     781 Lys 781
           |||
Db    2464 AAA 2466
```

RESULT 13
AAV58444
ID AAV58444 standard; DNA; 3266 BP.
XX
AC AAV58444;
XX
DT 02-DEC-1998 (first entry)
XX
DE Modified retinoblastoma tumour suppressor gene.
XX
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..2505
FT /*tag= a
XX
PN WO9837091-A2.
XX
PD 27-AUG-1998.
XX
PF 19-FEB-1998; 98WO-US03041.
XX
PR 20-FEB-1997; 97US-0038118.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Benedict WF, Hu S, Xu H, Zhou Y;
XX
DR WPI; 1998-480788/41.
DR P-PSDB; AAW69368.
XX
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
XX
PS Claim 22; Page 166-170; 249pp; English.
XX
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
XX
SQ Sequence 3266 BP; 1092 A; 602 C; 574 G; 998 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	3266
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-09-026-459A-37 (1-781) x AAV58444 (1-3266)

```
Qy      1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 219

Qy     21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 279

Qy     41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    280 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 339

Qy     61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    340 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 399

Qy     81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    400 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 459

      101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    460 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 519

Qy    121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    520 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 579

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    580 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 639

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    640 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 699

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    700 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 759

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    760 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 819

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    820 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 879

      241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    880 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 939

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    940 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 999

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1000 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1059

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1119

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1120 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1179

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1180 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1239

Qy    361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1240 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1299

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1300 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1359

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1419

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1479

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1539

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1599

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1659

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1719

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1779

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1839

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1899

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1959

Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2019

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2079

Qy    641 SerProTyrLysProProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2139

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2199

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2259

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2319

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2379

Qy     741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2439

Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2499

Qy     781 Lys 781
          |||
Db    2500 AAA 2502

RESULT 14
AAV58443
ID   AAV58443 standard; DNA; 3323 BP.
XX
AC   AAV58443;
XX
DT   02-DEC-1998  (first entry)
XX
DE   Modified retinoblastoma tumour suppressor gene.
XX
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7..2562
FT                   /*tag=  a
XX
PN   WO9837091-A2.
XX
PD   27-AUG-1998.
XX
PF   19-FEB-1998;   98WO-US03041.
XX
PR   20-FEB-1997;   97US-0038118.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Benedict WF,  Hu S,  Xu H,  Zhou Y;
XX
DR   WPI; 1998-480788/41.
DR   P-PSDB; AAW69367.
XX
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
XX
PS   Claim 22; Page 158-162; 249pp; English.
XX
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
XX
SQ   Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T; 0 other;

Alignment Scores:
Pred. No.:              0              Length:          3323
Score:                  4017.00        Matches:         781
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     19             Gaps:            0

US-09-026-459A-37 (1-781) x AAV58443 (1-3323)
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Qy       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     217 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 276

Qy      21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     277 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 336

Qy      41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     337 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 396

Qy      61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     397 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 456

Qy      81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     457 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 516

Qy     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     517 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 576

Qy     121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     577 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 636

Qy     141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     637 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 696

Qy     161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     697 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 756

Qy     181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     757 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 816

Qy     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     817 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 876

Qy     221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     877 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 936

Qy     241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     937 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 996

Qy     261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     997 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1056

Qy     281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1057 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1116

Qy     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1117 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1176

Qy     321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1177 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1236

Qy     341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1237 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1296
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Qy     361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1297 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1356

Qy     381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1357 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1416

Qy     401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1417 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1476

Qy     421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1477 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1536

Qy     441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1537 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1596

Qy     461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1597 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1656

Qy     481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1657 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1716

Qy     501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1717 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1776

Qy     521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1777 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1836

Qy     541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1837 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1896

Qy     561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1897 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1956

Qy     581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1957 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2016

Qy     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2017 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2076

Qy     621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2077 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2136

Qy     641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2137 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2196

Qy     661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2197 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2256

Qy     681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2257 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2316

Qy     701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2317 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2376

Qy     721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2377 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2436

Qy     741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2437 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2496

Qy     761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2497 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2556

Qy     781 Lys 781
           |||
Db    2557 AAA 2559
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RESULT 15
AAV58446
ID AAV58446 standard; DNA; 3323 BP.
XX
AC AAV58446;
XX
DT 02-DEC-1998 (first entry)
XX
DE Modified retinoblastoma tumour suppressor gene.
XX
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..2562
FT /*tag= a
XX
PN WO9837091-A2.
XX
PD 27-AUG-1998.
XX
PF 19-FEB-1998; 98WO-US03041.
XX
PR 20-FEB-1997; 97US-0038118.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Benedict WF, Hu S, Xu H, Zhou Y;
XX
DR WPI; 1998-480788/41.
DR P-PSDB; AAW69370.
XX
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
XX
PS Claim 22; Page 180-184; 249pp; English.
XX
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
XX
SQ Sequence 3323 BP; 1099 A; 647 C; 588 G; 989 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	3323
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-09-026-459A-37 (1-781) x AAV58446 (1-3323)

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Qy      1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 276

Qy     21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 336

Qy     41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 GCATTGGTGCTAAAAGTTTCTTCGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 396

Qy     61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    397 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 456

Qy     81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 516

Qy    101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    517 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 576

Qy    121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 636

Qy    141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    637 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 696

Qy    161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    697 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 756

Qy    181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    757 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 816

Qy    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    817 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 876

Qy    221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    877 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 936

Qy    241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    937 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 996

Qy    261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    997 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1056

Qy    281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1057 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1116

Qy    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1117 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1176

Qy    321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1177 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1236

Qy    341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1237 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1296

Qy    361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1297 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1356

Qy    381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1357 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1416

Qy    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1417 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1476

Qy    421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1477 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1536

Qy    441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1537 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1596

Qy    461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1597 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1656

Qy    481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1657 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1716

Qy    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1717 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1776

Qy    521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1777 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1836

Qy    541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1837 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1896

Qy    561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1897 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1956

Qy    581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1957 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2016

Qy    601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2017 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2076

Qy    621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2077 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2136

Qy    641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2137 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2196

Qy    661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2197 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2256

Qy    681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2257 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2316

Qy    701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2317 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2376

Qy    721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2377 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2436

Qy    741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2437 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2496

Qy    761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2497 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2556

Qy    781 Lys 781
          |||
Db   2557 AAA 2559


Search completed: January 18, 2003, 08:41:34
Job time : 305.854 secs
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